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(21) International Application Number: PCT/US98/11384 (22) International Filing Date: 1 June 1998 (01.06.98) (30) Priority Data: 08/868,373 3 June 1997 (03.06.97) US (71) Applicant (for all designated States except US): CARGILL, INCORPORATED [US/US]; 10547 West McGinty Road, Wayzata, MN 55391 (US). (71)(72) Applicants and Inventors: JAWORSKI, Jan, G. [US/US]; 425 Emerald Woods Drive, Oxford, OH 45058 (US). POST-BEITTENMILLER, Martha, Ann [US/US]; 2375 Quail Road, Ardmore, OH 73491 (US). TODD, James [US/US]; 17 Kelly Drive, Oxford, OH 45056 (US). (74) Agent: LUNDQUIST, Ronald, C.; Fish & Richardson P.C., P.A., Suite 3300, 60 South Sixth Street, Minneapolis, MN 55402 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: FATTY ACID ELONGASES (57) Abstract Nucleic acids are disclosed that encode fatty acid β -keto acyl synthases from plants. Such synthases are effective for producing very long chain fatty acids (VLCFA), e.g., C22 to C26, preferentially saturated but also monounsaturated. Also disclosed are polypeptides encoded by such nucleic acids. Transgenic plants expressing these polypeptides exhibit altered levels of VLCFA in one or more tissues, such as seeds or leaves.		

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FATTY ACID ELONGASESField of the Invention

5 This invention relates to fatty acid elongase complexes and nucleic acids encoding elongase proteins. More particularly, the invention relates to nucleic acids encoding β -keto acyl synthase proteins that are effective for producing very long chain fatty acids, polypeptides
10 produced from such nucleic acids and transgenic plants expressing such nucleic acids.

Background of the Invention

Plants are known to synthesize very long chain fatty acids (VLCFAs). VLCFAs are saturated or
15 unsaturated monocarboxylic acids with an unbranched even-numbered carbon chain that is greater than 18 carbons in length. Many VLCFAs are 20-32 carbons in length, but VLCFAs can be up to 60 carbons in length. Important VLCFAs include erucic acid (22:1, i.e., a 22 carbon chain
20 with one double bond), nervonic acid (24:1), behenic acid (22:0), and arachidic acid (20:0).

Plant seeds accumulate mostly 16- and 18-carbon fatty acids. VLCFAs are not desirable in edible oils. Oilseeds of the *Crucifereae* (e.g., rapeseed) and a few
25 other plants, however, accumulate C20 and C22 fatty acids (FAs). Although plant breeders have developed rapeseed lines that have low levels of VLCFAs for edible oil purposes, even lower levels would be desirable. On the other hand, vegetable oils having elevated levels of
30 VLCFAs are desirable for certain industrial uses, including uses as lubricants, fuels and as a feedstock for plastics, pharmaceuticals and cosmetics.

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The biosynthesis of saturated fatty acids up to an 18-carbon chain occurs in the chloroplast. C2 units from acyl thioesters are linked sequentially, beginning with the condensation of acetyl Coenzyme A (CoA) and malonyl acyl carrier protein (ACP) to form a C4 acyl fatty acid. This condensation reaction is catalyzed by a β -ketoacyl synthase III (KASIII). β -ketoacyl moieties are also referred to as 3-ketoacyl moieties.

The enzyme β -ketoacyl synthase I (KASI) is involved in the addition of C2 groups to form the C6 to C16 saturated fatty acids. KASI catalyzes the stepwise condensation of a fatty acyl moiety (C4 to C14) with malonyl-ACP to produce a 3-ketoacyl-ACP product that is 2 carbons longer than the substrate. The last condensation reaction in the chloroplast, converting C16 to C18, is catalyzed by β -ketoacyl synthase II (KASII).

Each elongation cycle involves three additional enzymatic steps in addition to the condensation reaction as discussed above. Briefly, the β -ketoacyl condensation product is reduced to β -hydroxyacyl-ACP, dehydrated to the enoyl-ACP, and finally reduced to a fully reduced acyl-ACP. The fully reduced fatty acyl-ACP reaction product then serves as the substrate for the next cycle of elongation.

The C18 saturated fatty acid (stearic acid, 18:0) can be transported out of the chloroplast and converted to the monounsaturate C18:1 (oleic acid), and the polyunsaturates C18:2 (linoleic acid) and C18:3 (α -linolenic acid). C18:0 and C18:1 can also be elongated outside the chloroplast to form VLCFAs. The formation of VLCFAs involves the sequential condensation of two carbon groups from malonyl CoA with a C18:0 or C18:1 fatty acid substrate. Elongation of fatty acids longer than 18 carbons depends on the activity of a fatty acid elongase complex to carry out four separate enzyme reactions

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similar to those described above for fatty acid synthesis in the chloroplast. Fehling, Biochem. Biophys. Acta 1082:239-246 (1991). In plants, elongase complexes are distinct from fatty acid synthases since elongases are
5 extraplasmidial and membrane bound.

Mutations have been identified in an Arabidopsis gene associated with fatty acid elongation. This gene, designated the *FAE1* gene, is involved in the condensation step of an elongation cycle. See, WO 96/13582,
10 incorporated herein by reference. Plants carrying a mutation in *FAE1* have significant decreases in the levels of VLCFAs in seeds. Genes associated with wax biosynthesis in jojoba have also been cloned and sequenced (WO 95/15387, incorporated herein by
15 reference).

Very long chain fatty acids are key components of many biologically important compounds in animals, plants, and microorganisms. For example, in animals, the VLCFA arachidonic acid is a precursor to many prostaglandins.
20 In plants VLCFAs are major constituents of triacylglycerols in many seed oils, are essential precursors for cuticular wax production, and are utilized in the synthesis of glycosylceramides, an important component of the plasma membrane.

25 Obtaining detailed information on the biochemistry of KAS enzymes has been hampered by the difficulties encountered when purifying membrane bound enzymes. Although elongase activities have been partially purified from a number of sources, or studied using cell
30 fractions, the elucidation of the biochemistry of elongase complexes has been hampered by the complexity of the membrane fractions used as the enzyme source. For example, until recently, it was unclear as to whether plant elongase complexes were composed of a
35 multifunctional polypeptide similar to the FAS found in

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animals and yeast, or if the complexes existed as discrete and dissociable enzymes similar to the FAS of plants and bacteria. Partial purification of an elongase KAS, immunoblot identification of the hydroxy acyl
5 dehydrase, and the recent cloning of a KAS gene (FAE1) suggest that the enzyme activities of elongase complexes exist on individual enzymes.

Summary of the Invention

The invention disclosed herein relates to an
10 isolated polynucleotide selected from one of the following: SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; an RNA analog of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or 15; and a polynucleotide having a nucleic acid sequence
15 complementary to one of the above. The polynucleotide can also be a nucleic acid fragment of one of the above sequences that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ
20 ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

Also disclosed herein is an isolated polypeptide that has an amino acid sequence substantially identical to one of the following: SEQ ID NO:2, SEQ ID NO:4, SEQ ID
25 NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14. Also disclosed are isolated polynucleotides encoding polypeptides substantially identical in their amino acid sequence to: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID
30 NO:14.

The invention also relates to a transgenic plant containing a nucleic acid construct. The nucleic acid construct comprises a polynucleotide described above. The construct further comprises a regulatory element

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operably linked to the polynucleotide. The regulatory element may a tissue-specific promoter, for example, an epidermal cell-specific promoter or a seed-specific promoter. The regulatory element may be operably linked
5 to the polynucleotide in sense or antisense orientation. The plant has altered levels of very long chain fatty acids in tissues where the polynucleotide is expressed, compared to a parental plant lacking the nucleic acid construct.

10 A method is disclosed for altering the levels of very long chain fatty acids in a plant. The method comprises the steps of creating a nucleic acid construct and introducing the construct into the plant. The construct includes a polynucleotide selected from one of
15 the following: SEQ ID NO:1; SEQ ID NO:3; SEQ ID NO:5; SEQ ID NO:7; SEQ ID NO:9; SEQ ID NO:11; SEQ ID NO:13; an RNA analog of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or 15; and a polynucleotide having a nucleic acid sequence complementary to one of the above. The polynucleotide
20 can also be a nucleic acid fragment of one of the above that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ
25 ID NO:14. The polynucleotide is effective for altering the levels of very long chain fatty acids in the plant.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

30 Brief Description of the Drawings

Figure 1 shows the time course of *in vitro* VLCFA synthesis by FAE1 expressed in yeast, with 3 different acyl-CoA substrates.

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Figure 2 shows the rates of *in vitro* VLCFA synthesis and the VLCFA profiles of FAE1 expressed in yeast, with 3 different acyl-CoA substrates.

Figure 3 shows the nucleotide sequence of the
5 coding region of the *Arabidopsis* EL1 polynucleotide (SEQ ID NO:1).

Figure 4 shows the deduced amino acid sequence (SEQ ID NO:2) for the EL1 coding sequence of Figure 3.

Figure 5 shows the nucleotide sequence of the
10 coding region of the *Arabidopsis* EL2 polynucleotide (SEQ ID NO:3).

Figure 6 shows the deduced amino acid sequence (SEQ ID NO:4) for the EL2 coding sequence of Figure 5.

Figure 7 shows the nucleotide sequence of the
15 coding region of the *Arabidopsis* EL3 polynucleotide (SEQ ID NO:5).

Figure 8 shows the deduced amino acid sequence (SEQ ID NO:6) for the EL3 coding sequence of Figure 7.

Figure 9 shows the nucleotide sequence of the
20 coding region of the *Arabidopsis* EL4 polynucleotide (SEQ ID NO:7).

Figure 10 shows the deduced amino acid sequence (SEQ ID NO:8) for the EL4 coding sequence of Figure 9.

Figure 11 shows the nucleotide sequence of the
25 coding region of the *Arabidopsis* EL5 polynucleotide (SEQ ID NO:9).

Figure 12 shows the deduced amino acid sequence (SEQ ID NO:10) for the EL5 coding sequence of Figure 11.

Figure 13 shows the nucleotide sequence of the
30 coding region of the *Arabidopsis* EL6 polynucleotide (SEQ ID NO:11).

Figure 14 shows the deduced amino acid sequence (SEQ ID NO:12) for the EL6 coding sequence of Figure 13.

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Figure 15 shows the nucleotide sequence of the coding region of the Arabidopsis EL7 polynucleotide (SEQ ID NO:13).

Figure 16 shows the deduced amino acid sequence
5 (SEQ ID NO:14) for the EL7 coding sequence of Figure 15.

Description of the Preferred Embodiments

The present invention comprises isolated nucleic acids (polynucleotides) that encode polypeptides having β -ketoacyl synthase activity. The novel polynucleotides
10 and polypeptides of the invention are involved in the synthesis of very long chain fatty acids and are useful for modulating the total amounts of such fatty acids and the specific VLCFA profile in plants.

A polynucleotide of the invention may be in the
15 form of RNA or in the form of DNA, including cDNA, synthetic DNA or genomic DNA. The DNA may be double-stranded or single-stranded, and if single-stranded, can be either the coding strand or non-coding strand. An RNA analog may be, for example, mRNA or a combination of
20 ribo- and deoxyribonucleotides. Illustrative examples of a polynucleotide of the invention are shown in Figs. 3, 5, 7, 9, 11, 13 and 15.

A polynucleotide of the invention typically is at least 15 nucleotides (or base pairs, bp) in length. In
25 some embodiments, a polynucleotide is about 20 to 100 nucleotides in length, or about 100 to 500 nucleotides in length. In other embodiments, a polynucleotide is greater than about 1500 nucleotides in length and encodes a polypeptide having the amino acid sequence shown in
30 Figs. 4, 6, 8, 10, 12, 14 or 16.

In some embodiments, a polynucleotide of the invention encodes analogs or derivatives of a polypeptide having the deduced amino acid sequence of Figs. 4, 6, 8,

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10, 12, 14 or 16. Such fragments, analogs or derivatives include, for example, naturally occurring allelic variants, non-naturally occurring allelic variants, deletion variants and insertion variants, that do not
5 substantially alter the function of the polypeptide.

A polynucleotide of the invention may further comprise additional nucleic acids. For example, a nucleic acid fragment encoding a secretory or leading amino acid sequence can be fused in-frame to the amino
10 terminal end of one of the EL1 through EL7 polypeptides. Other nucleic acid fragments are known in the art that encode amino acid sequences useful for fusing in-frame to the KAS polypeptides disclosed herein. See, e.g., U.S. 5,629,193 incorporated herein by reference. A
15 polynucleotide may further comprise one or more regulatory elements operably linked to a KAS polynucleotide disclosed herein.

The present invention also comprises polynucleotides that hybridize to a KAS polynucleotide
20 disclosed herein. Such a polynucleotide typically is at least 15 nucleotides in length. Hybridization typically involves Southern analysis (Southern blotting), a method by which the presence of DNA sequences in a target nucleic acid mixture are identified by hybridization to a
25 labeled oligonucleotide or DNA fragment probe. Southern analysis typically involves electrophoretic separation of DNA digests on agarose gels, denaturation of the DNA after electrophoretic separation, and transfer of the DNA to nitrocellulose, nylon, or another suitable membrane
30 support for analysis with a radiolabeled, biotinylated, or enzyme-labeled probe as described in sections 9.37-9.52 of Sambrook et al., (1989) *Molecular Cloning*, second edition, Cold Spring Harbor Laboratory, Plainview; NY.

A polynucleotide can hybridize under moderate
35 stringency conditions or, preferably, under high

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stringency conditions to a KAS polynucleotide disclosed herein. High stringency conditions are used to identify nucleic acids that have a high degree of homology to the probe. High stringency conditions can include the use of
5 low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate (0.1X SSC); 0.1% sodium lauryl sulfate (SDS) at 65°C. Alternatively, a denaturing agent such as formamide can be employed during hybridization, e.g., 50% formamide with 0.1%
10 bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C. Another example is the use of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium
15 phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS.

Moderate stringency conditions refers to
20 hybridization conditions used to identify nucleic acids that have a lower degree of identity to the probe than do nucleic acids identified under high stringency conditions. Moderate stringency conditions can include the use of higher ionic strength and/or lower
25 temperatures for washing of the hybridization membrane, compared to the ionic strength and temperatures used for high stringency hybridization. For example, a wash solution comprising 0.060 M NaCl/0.0060 M sodium citrate (4X SSC) and 0.1% sodium lauryl sulfate (SDS) can be used
30 at 50°C, with a last wash in 1X SSC, at 65°C. Alternatively, a hybridization wash in 1X SSC at 37°C can be used.

Hybridization can also be done by Northern analysis (Northern blotting), a method used to identify
35 RNAs that hybridize to a known probe such as an

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oligonucleotide, DNA fragment, cDNA or fragment thereof,
or RNA fragment. The probe is labeled with a
radioisotope such as ^{32}P , by biotinylation or with an
enzyme. The RNA to be analyzed can be usually
5 electrophoretically separated on an agarose or
polyacrylamide gel, transferred to nitrocellulose, nylon,
or other suitable membrane, and hybridized with the
probe, using standard techniques well known in the art
such as those described in sections 7.39-7.52 of Sambrook
10 et al., *supra*.

A polynucleotide has at least about 70% sequence
identity, preferably at least about 80% sequence
identity, more preferably at least about 90% sequence
identity to SEQ ID NO:1, 3, 5, 7, 9, 11, or 13. Sequence
15 identity can be determined, for example, by computer
programs designed to perform single and multiple sequence
alignments.

A polynucleotide of the invention can be obtained
by chemical synthesis, isolation and cloning from plant
20 genomic DNA or other means known to the art, including
the use of PCR technology carried out using
oligonucleotides corresponding to portions of SEQ ID
NO:1, 3, 5, 7-9, 11 or 13. Polymerase chain reaction
(PCR) refers to a procedure or technique in which target
25 nucleic acid is amplified in a manner similar to that
described in U.S. Patent No. 4,683,195, incorporated
herein by reference, and subsequent modifications of the
procedure described therein. Generally, sequence
information from the ends of the region of interest or
30 beyond is employed to design oligonucleotide primers that
are identical or similar in sequence to opposite strands
of the template to be amplified. PCR can be used to
amplify specific RNA sequences, specific DNA sequences
from total genomic DNA, and cDNA transcribed from total
35 cellular RNA, bacteriophage or plasmid sequences, and the

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like. Alternately, a cDNA library (in an expression vector) can be screened with KAS-specific antibody prepared using peptide sequence(s) from hydrophilic regions of the KAS protein of SEQ ID NO:2 and technology
5 known in the art.

A polypeptide of the invention comprises an isolated polypeptide having the deduced amino acid sequence of Figs. 2, 4, 6, 8, 10 and 12, as well as derivatives and analogs thereof. By "isolated" is meant
10 a polypeptide that is expressed and produced in an environment other than the environment in which the polypeptide is naturally expressed and produced. For example, a plant polypeptide is isolated when expressed and produced in bacteria or fungi. Similarly, a plant
15 polypeptide is isolated when its gene coding sequence is operably linked to a chimeric regulatory element and expressed in a tissue where the polypeptide is not naturally expressed. A polypeptide of the invention also comprises variants of the KAS polypeptides disclosed
20 herein, as discussed above.

A full-length KAS coding sequence may comprise the sequence shown in SEQ ID NO:1, 3, 5, 7, 9, 11 or 13. Alternatively, a chimeric full-length KAS coding sequence may be formed by linking, in-frame, nucleotides from the
25 5' region of a first KAS gene to nucleotides from the 3' region of a second KAS gene, thereby forming a chimeric KAS protein.

It should be appreciated that nucleic acid fragments having a nucleotide sequence other than the KAS
30 sequences disclosed in SEQ ID NO:1, 3, 5, 7, 9, 11 or 13 will encode a polypeptide having the exemplified amino acid coding sequence of SEQ ID NO:2, 4, 6, 8, 10, 12 or 14, respectively. The degeneracy of the genetic code is well-known to the art; i.e., for many amino acids, there

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is more than one nucleotide triplet which serves as the codon for the amino acid.

It should also be appreciated that certain amino acid substitutions can be made in protein sequences without affecting the function of the protein. Generally, conservative amino acid substitutions or substitutions of similar amino acids are tolerated without affecting protein function. Similar amino acids can be those that are similar in size and/or charge properties, for example, aspartate and glutamate and isoleucine and valine are both pairs of similar amino acids. Similarity between amino acid pairs has been assessed in the art in a number of ways. For example, Dayhoff et al. (1978) in *Atlas of Protein Sequence and Structure*, Vol. 5, Suppl. 3, pp. 345-352, which is incorporated by reference herein, provides frequency tables for amino acid substitutions which can be employed as a measure of amino acid similarity.

A nucleic acid construct of the invention comprises a polynucleotide as disclosed herein linked to another, different polynucleotide. For example, a full-length KAS coding sequence may be operably fused in-frame to a nucleic acid fragment that encodes a leader sequence, secretory sequence or other additional amino acid sequences that may be usefully linked to a polypeptide or peptide fragment.

A transgenic plant of the invention contains a nucleic acid construct as described herein. In some embodiments, a transgenic plant contains a nucleic acid construct that comprises a polynucleotide of the invention operably linked to at least one suitable regulatory sequence in sense orientation. Regulatory sequences typically do not themselves code for a gene product. Instead, regulatory sequences affect the expression level of the polynucleotide to which they are

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linked. Examples of regulatory sequences are known in the art and include, without limitation, minimal promoters and promoters of genes preferentially or exclusively expressed in seeds or in epidermal cells of stems and leaves. Native regulatory sequences of the polynucleotides disclosed herein can be readily isolated by those skilled in the art and used in constructs of the invention. Other examples of suitable regulatory sequences include enhancers or enhancer-like elements, introns, 3' non-coding regions such as poly A sequences and other regulatory sequences discussed herein. Molecular biology techniques for preparing such chimeric genes are known in the art.

In other embodiments, a transgenic plant contains a nucleic acid construct comprising a partial or a full-length KAS coding sequence operably linked to at least one suitable regulatory sequence in antisense orientation. The chimeric gene can be introduced into a plant and transgenic progeny displaying expression of the antisense construct are identified.

One may use a polynucleotide disclosed herein for cosuppression as well as for antisense inhibition. Cosuppression of genes in plants may be achieved by expressing, in the sense orientation, the entire or partial coding sequence of a gene. See, e.g., WO 04/11516, incorporated herein by reference.

Transgenic techniques for use in the invention include, without limitation, *Agrobacterium*-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation. Illustrative examples of transformation techniques are described in U.S. Patent 5,204,253, (particle gun) and U.S. Patent 5,188,958 (*Agrobacterium*), incorporated herein by reference. Transformation methods utilizing the Ti and Ri plasmids of *Agrobacterium* spp. typically

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use binary-type vectors. Walkerpeach, C. et al., in Plant Molecular Biology Manual, S. Gelvin and R. Schilperoort, eds., Kluwer Dordrecht, C1:1-19 (1994). If cell or tissue cultures are used as the recipient tissue
5 for transformation, plants can be regenerated from transformed cultures by techniques known to those skilled in the art.

Techniques are known for the introduction of DNA into monocots as well as dicots, as are the techniques
10 for culturing such plant tissues and regenerating those tissues. Monocots which have been successfully transformed and regenerated include wheat, corn, rye, rice, and asparagus. See, e.g., U.S. Patent Nos. 5,484,956 and 5,550,318, incorporated herein by
15 reference.

For efficient production of transgenic plants from plant cells, it is desirable that the plant tissue used for transformation possess a high capacity for regeneration. Transgenic plants of woody species such as
20 poplar and aspen have also been obtained. Technology is also available for the manipulation, transformation, and regeneration of gymnosperm plants. For example, U.S. Patent No. 5,122,466 describes the biolistic transformation of conifers, with preferred target tissue
25 being meristematic and cotyledon and hypocotyl tissues. U.S. Patent No. 5,041,382 describes enrichment of conifer embryonal cells.

Seeds produced by a transgenic plant(s) can be grown and then selfed (or outcrossed and selfed) to
30 obtain seeds homozygous for the construct. Seeds can be analyzed in order to identify those homozygotes having the desired expression of the construct. Transgenic plants may be entered into a breeding program, e.g., to introgress the novel construct into other lines, to
35 transfer the construct to other species, or for further

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selection of other desirable traits. Alternatively, transgenic plants may be propagated vegetatively for those species amenable to such techniques. A nucleic acid construct of the invention can alter the levels of very long chain fatty acids in plant tissues expressing the polynucleotide, compared to VLCFA levels in corresponding tissues from an otherwise identical plant not expressing the polynucleotide. A comparison can be made, for example, between a non-transgenic plant of a plant line and a transgenic plant of the same plant line. Levels of VLCFAs having 20-32 carbons and/or levels of VLCFAs having 32-60 carbons can be altered in plants disclosed herein. Plants having an altered VLCFA composition may be identified by techniques known to the skilled artisan, e.g., thin layer chromatography or gas-liquid chromatography (GLC) analysis of the appropriate plant tissue.

A suitable group of plants with which to practice the invention are the *Brassica* species, including *B. napus*, *B. rapa*, *B. juncea*, and *B. hirta*. Other suitable plants include, without limitation, soybean (*Glycine max*), sunflower (*Helianthus annuus*) and corn (*Zea mays*).

A method according to the invention comprises introducing a nucleic acid construct into a plant cell and producing a plant (as well as progeny of such a plant) from the transformed cell. Progeny includes descendants of a particular plant or plant line, e.g., seeds developed on an instant plant are descendants. Progeny of an instant plant include seeds formed on F_1 , F_2 , F_3 , and subsequent generation plants, or seeds formed on BC_1 , BC_2 , BC_3 , and subsequent generation plants.

Methods and compositions according to the invention are useful in that the resulting plants and plant lines have desirable alterations in very long chain fatty acid composition. Suitable tissues in which to

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express polynucleotides and/or polypeptides of the invention include, without limitation, seeds, stems and leaves. Leaf tissues of interest include cells and tissues of the epidermis, e.g., cells that are involved
5 in forming trichomes. Of particular interest are epidermal cells involved in forming the cuticular layer. The cuticular layer comprises various very long chain fatty acids and VLCFA derivatives such as alkanes, esters, alcohols and aldehydes. Altering the composition
10 and amount of VLCFAs in epidermal cells and tissues may enhance defense mechanisms and drought tolerance of plants disclosed herein.

Polynucleotides of the invention can be used as markers in plant genetic mapping and plant breeding
15 programs. Such markers may include RFLP, RAPD, or PCR markers, for example. Marker-assisted breeding techniques may be used to identify and follow a desired fatty acid composition during the breeding process. Marker-assisted breeding techniques may be used in
20 addition to, or as an alternative to, other sorts of identification techniques. An example of marker-assisted breeding is the use of PCR primers that specifically amplify a sequence from a desired KAS that has been introduced into a plant line and is being crossed into
25 other plant lines.

Plants and plant lines disclosed herein preferably have superior agronomic properties. Superior agronomic characteristics include, for example, increased seed germination percentage, increased seedling vigor,
30 increased resistance to seedling fungal diseases (damping off, root rot and the like), increased yield, and improved standability.

While the invention is susceptible to various modifications and alternative forms, certain specific
35 embodiments thereof are described in the general methods

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and examples set forth below. It should be understood, however, that these examples are not intended to limit the invention to the particular forms disclosed but, instead the invention is to cover all modifications, 5 equivalents and alternatives falling within the scope of the invention.

EXAMPLES

Example 1

Cloning and Expression of FAE1 in Yeast Cells

10 The open reading frame of the *Arabidopsis* FAE1 gene was amplified directly by PCR, using *Arabidopsis thaliana* cv. Columbia genomic DNA as a template, pfu DNA polymerase and the following primers:

5'CTCGAGGAGCAATGACGTCCGTTAA-3' and 5'-

15 CTCGAGTTAGGACCGACCGTTTGTG-3'. The PCR product was blunt-end cloned into the *Eco* RV site of pBluescript (Stratagene, La Jolla, CA),

 The FAE1 gene was excised from the Bluescript vector with *Bam*HI, and then subcloned into the pYEura3 20 (Clontech, Palo Alto, CA). pYEura3 is a yeast centromere-containing, episomal plasmid that is propagated stably through cell division. The FAE1 gene was inserted downstream of a GAL1 promoter in pYEura3. The GAL1 promoter is induced when galactose is present in 25 the medium and repressed when glucose is present in the growth medium.

 Insertion of the FAE1 gene in the sense orientation was confirmed by PCR, and pYEura3/FAE1 was used to transform *Saccharomyces cerevisiae* strain AB1380 30 using a lithium acetate procedure as described in Gietz, R. and Woods, R., in *Molecular Genetics of Yeast: Practical Approaches*, Oxford Press, pp. 121-134 (1994). Plasmid DNA was isolated from putative transformants, and

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the presence of the *FAE1*/pYEUra3 construct was confirmed by Southern analysis.

Yeast transformed with pYEUra3 having *FAE1* operably linked to the *GAL1* promoter were grown in the presence of galactose or glucose and were analyzed for the expression of *FAE1*. As a control, yeast transformed with pYEUra3 containing no insert were also assayed. Analysis of such control preparations yielded fatty acid compositions and fatty acid elongation rates similar to those of yeast transformed with pYEUra3/*FAE1* and grown with glucose as the carbon source.

The fatty acid composition of yeast cells grown in the presence of galactose was compared to that of cells grown in the presence of glucose, to determine if VLCFA were found in the galactose-induced cells.

Transformed yeast cells were grown overnight in YPD media at 30°C with vigorous shaking. One hundred μ l of the overnight culture were used to inoculate 40 ml of complete minimal uracil dropout media (CM-Ura) supplemented with either glucose or galactose (2% w/v). Cultures were grown at 30°C to an OD₆₀₀ of approximately 1.3 to 1.5. Cells were harvested by centrifugation at 5000 Xg for 10 min. Total lipids were extracted from the cells with 2 volumes of 4N KOH in 100% methanol for 60 min. at 80°C. Fatty acids were saponified and methyl esters were prepared by drying the samples and resuspending in 0.5 ml of boron trichloride in methanol (10% v/v). Samples were incubated at 50°C for 15 min in a sealed tube. About 2 ml of water was then added and the fatty methyl esters were extracted thrice with 1 ml of hexane. Extracts were dried under nitrogen and redissolved in hexane. See Hlousek-Radojcic, A. et al., Plant J. 8:803-809. Methyl esters were analyzed on an HP 5890 series II gas chromatograph equipped with a 5771MSD and 7673 auto injector (Hewlett-Packard, Cincinnati, OH).

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Methyl esters were separated on a DB-23 (J&W Scientific) capillary column (30 m X 0.25 mm X 0.25 μ m). The column was operated with helium carrier gas and splitless injection (injection temperature 280°C, detector temperature 280°C). After an initial 3 min. at 100°C, the oven temperature was raised to 250° at 20°C min⁻¹ and maintained at that temperature for an additional 3 min. The identity of the peaks was verified by cochromatography with authentic standards and by mass spectrometer analysis.

The results clearly revealed the appearance of both 20:1 and 22:1 acyl-CoA products in galactose-induced yeast containing the *FAE1* coding sequence. Uninduced yeast cells failed to accumulated significant amounts of fatty acids longer than C18. These results indicate that expression of *FAE1* in yeast resulted in functional KAS activity and functional elongase activity.

Example 2

***FAE1* Activity in Yeast Microsomes**

The functional expression of the *FAE1* KAS was analyzed by isolating microsomes from transformed yeast cells and assaying these microsomes *in vitro* for elongase activity.

Transformed yeast cells were grown in the presence of either glucose or galactose (2% w/v) as described in Example 1. Cells were harvested by centrifugation at 5000 Xg for 10 min and washed with 10 ml ice cold isolation buffer (IB), which contains 80 mM Hepes-KOH, pH 7.2, 5 mM EGTA, 5 mM EDTA, 10 mM KCl, 320 mM sucrose and 2 mM DTT). Cells were then resuspended in enough IB to fill a 1.7 ml tube containing 700 μ l of 0.5 μ m glass beads and yeast microsomes were isolated from the cells essentially as described in Tillman, T. and Bell, R., J. Biol. Chem. 261:9144-9149 (1986). The microsomal

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membrane pellet was recovered by centrifugation at 252,000 xg for 60 min. The pellet was rinsed by resuspending in 40 ml fresh IB and again recovered by centrifugation at 252000 Xg for 60 min. Microsomal
5 pellets were resuspended in a minimal volume of IB, and the protein concentration adjusted to $2.5 \mu\text{g } \mu\text{l}^{-1}$ by addition of IB containing 15% glycerol. Microsomes were frozen on dry ice and stored at -80°C . The protein concentration in microsomes was determined by the
10 Bradford method (Bradford, 1976).

Fatty acid elongase activity was measured essentially as described in Hlousek-Radojcic, A. et al., Plant J. 8:803-809 (1995). Briefly, the standard elongation reaction mix contained 80 mM Hepes-KOH, pH
15 7.2, 20 mM MgCl_2 , 500 μM NADPH, 1 mM ATP, 100 μM malonyl-CoA, 10 μM CoA-SH and 15 μM radioactive acyl-CoA substrate. The radiolabeled substrate was either $[1\text{-}^{14}\text{C}]18:1\text{-CoA}$ (50 $\text{uCi } \mu\text{mol}^{-1}$), $[1\text{-}^{14}\text{C}]18:0\text{-CoA}$ (55 $\text{uCi } \mu\text{mol}^{-1}$), or $[1\text{-}^{14}\text{C}]16:0\text{-CoA}$ (54 $\text{uCi } \mu\text{mol}^{-1}$). The reaction was
20 initiated by the addition of yeast microsomes (5 μg protein) and the mixture incubated at 30°C for the indicated period of time. The final reaction volume was 25 μl .

Methyl esters of the acyl-CoA elongation products
25 were prepared as described in Example 1. Methyl esters were separated on reversed phase silica gel KC18 TLC plates (Whatman, 250 μM thick), quantified by phosphorimaging, and analyzed on by ImageQuant software (Molecular Dynamics, Inc., Sunnyvale, CA). The detection
30 limit for each product is about 0.001 nanomoles per min. per mg microsomal protein, depending on the phosphorimage exposure time.

Results of representative *in vitro* elongation assays are shown in Figs. 1 and 2. The results indicate
35 that microsomes from galactose-induced cells expressing

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FAE1 catalyzed multiple cycles of elongation starting with either C16:0 acyl CoA, C18:0 acyl CoA, or C18:1 acyl-CoA as the substrate (Fig. 1). The 16:0 and 18:0 acyl-CoA substrates were elongated to C26:0 acyl-CoA. In contrast, the 18:1-CoA substrate was elongated primarily to C20:1, with only low levels of C22:1 acyl-CoA being produced. Occasionally, trace levels of C24:1 CoA were also observed. Although the chain length of the products from the 18:1 acyl-CoA substrate were less than the chain length from the saturated acyl-CoA substrates, the rate of elongation of oleoyl-CoA was about 2- and 3-fold higher than the rates of elongation of 16:0-CoA and 18:0-CoA, respectively.

The elongation activity observed in microsomes from uninduced cells indicated that there was a low level of endogenous elongase activity when 18:1-CoA or 18:0-CoA were used as substrates. There was substantial 16:0-CoA elongase activity (10.1 nmol mg protein⁻¹ at 30 min) in microsomes from uninduced cells (Fig. 2). However, the major product of 16:0 elongation using uninduced microsomes was C18:0 acyl CoA, with only small amounts of products beyond this length. The elongation of the 16:0 acyl-CoA substrate presumably is due to an endogenous yeast elongase.

Elongation of 18:1 CoA by microsomes from induced cells occurred at a rate about 18-fold higher than in microsomes isolated from the uninduced cells (Fig. 2). With microsomes from induced yeast, synthesis of 20:0 CoA from the 16:0 CoA substrate, occurred at a rate similar to that seen when the substrate was 18:0 CoA (4.2 vs. 5.1 nmol mg protein⁻¹). The total rate of elongation of [¹⁴C] 16:0-CoA by microsomes from induced cells (15.8 nmol mg protein⁻¹ at 30 min.) was more than 50% higher than elongation of [¹⁴C] 16:0-CoA by microsomes from uninduced cells, suggesting that the *FAE1* KAS utilized 16:0-CoA as

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a substrate in addition to C18-C24 acyl-CoAs. The FAE1 elongase KAS activity, i.e., the difference in the 16:0 elongation rates between microsomes from induced and uninduced cells, was 5.7 nmol mg protein⁻¹. The
5 elongation rate with the 16:0 substrate thus was similar to the elongase activity of the FAE1 elongase KAS with the 18:0 substrate.

These results indicate that FAE1 KAS expressed in yeast could synthesize 3-ketoacyl-CoA *in vitro* and, in
10 combination with yeast reductases and dehydrases, could form a functional VLCFA elongase complex. In addition, these results suggest that FAE1 is membrane-bound in yeast cells.

Example 3

15 **Cloning and Sequencing of Arabidopsis Elongase Genes**

The sequence of a jojoba seed cDNA (see WO 93/10241 and WO 95/15387, incorporated herein by reference) was used to search the Arabidopsis expressed sequence tag (EST) database of the Arabidopsis Genome
20 Stock Center (The Ohio State University, Columbus, Ohio). The BLAST computer program (National Institutes of Health, Bethesda, MD, USA) was used to perform the search. The search identified two ESTs (ATTS1282 and ATTS3218) that had a high degree of sequence identity
25 with the jojoba sequence. The ATTS1282 and ATTS3218 ESTs appeared to be partial cDNA clones rather than full-length clones based on the length of the jojoba sequence.

A genomic DNA library from *Arabidopsis thaliana* cv. Columbia, was prepared in the lambda GEM11 vector
30 (Promega, Madison, Wisconsin) and was obtained from Ron Davis, Stanford University, Stanford, CA. The library was hybridized with ATTS1282 and ATTS3218 as probes and 2 clones were identified for each EST. Phage DNA was isolated from each of the hybridizing clones, the genomic

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insert was excised with the restriction enzyme Sac I and subcloned into the plasmid pBluescript (Stratagene, La Jolla, CA). One clone from the ATTS1282 hybridization was designated EL1 and one clone from the ATTS3218
5 hybridization was designated EL2.

A yeast expression library, containing cDNA from *Arabidopsis thaliana* cv. Columbia, was prepared in the lambda YES expression vector described in Elledge et al. (Elledge, S. et al., Proc. Natl. Acad. Sci USA 88:1731-
10 1735 (1991) and was obtained from Ron Davis at Stanford University, Stanford, CA. The library was hybridized with a EL2 partial cDNA probe. A full-length EL2 cDNA was not identified. However, the probe did identify a full-length cDNA which was designated EL3.

15 A consensus sequence for the C-terminal region of EL1, EL2 and the jojoba cDNA polypeptides was identified by sequence alignment using DNA analysis programs from DNASTar, Madison, Wisconsin. This consensus sequence was used to search the *Arabidopsis* EST database again for β -
20 keto acyl synthase sequences. These searches identified four additional putative β -keto acyl synthase ESTs, which were designated EL4 through EL7. EL4, EL5, EL6, and EL7 have homology to Genbank Accession Nos. T04345, T44939, T22193 and T76700, respectively.

25 The lambda YES cDNA expression library described above was hybridized with the EL1 and EL4-EL7 ESTs as probes. This screen identified full-length cDNAs for EL1, EL5 and EL6.

The lambda GEM11 genomic library was hybridized
30 with the EL4 and EL7 ESTs as probes. This screen identified full-length genomic clones for EL4 and EL7. Phage DNA was isolated from each of the hybridizing clones and subcloned into pBluescript as described above.

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The 7 EL clones were sequenced on both strands with regions of overlap for each sequence run. Sequencing was carried out with an ABI automated sequencer (Applied Biosystems, Inc., Foster City, California), following the manufacturer's instructions.

The nucleotide sequences for the coding regions of EL1-EL7 are shown in Figs. 3, 5, 7, 9, 11, 13 and 15, respectively. The deduced amino acid sequences for EL1-EL7 are shown in Figs. 4, 6, 8, 10, 12, 14 and 16, respectively, using the standard one-letter amino acid code. The EL1, EL2 and EL7 genomic clones appeared to lack introns. The EL4 genomic clone contained one intron near the 5' end of the coding region.

The nucleotide sequences of the 7 EL polynucleotides were compared to 5 DNA sequences present in Genbank. Genbank, National Center for Biotechnology Information, Bethesda, MD. Two of the 5 accessions were cloned from members of the Brassicaceae: the *Arabidopsis* FAEl sequence (Accession U29142) and a *Brassica napus* sequence (Accession U50771). Three of the accessions were cloned from jojoba (*Simmondsia chinensis*): 2 wax biosynthesis genes (Accessions I14084 and I14085) and a jojoba KAS gene (Accession U37088). See also U.S. Patent 5,445,947, incorporated herein by reference.

Multiple alignment of the 12 sequences was carried out with a computer program sold under the trade name MEGALIGN Lasergene by DNASTar (Madison, Wisconsin). Alignments were done using the Clustal method with weighted residue weight table. The nucleotide sequence similarity index and percent divergence based on the multiple alignment algorithm is shown in Table 1. The nucleotide sequences of EL1-EL7 are distinguishable from the 5 DNA sequences obtained from Genbank.

The deduced amino acid sequences of the EL1-7 polypeptides were compared with the MEGALIGN program to

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the deduced amino acid sequences of the same 5 Genbank clones, using the Clustal method with PAM250 residue weight table. The amino acid sequence similarity and percent divergence are shown in Table 2. The amino acid
5 sequences of EL1-EL7 polypeptides are distinguishable from those of the Genbank sequences.

TABLE 1

Nucleotide sequence pair distances of EL1-EL7, using Clustal method with weighted residue weight table.

	1	2	3	4	5	6	7	8	9	10	11	12	
1		77.5	62.4	58.8	57.0	54.9	47.0	42.8	42.9	43.1	44.7	41.3	1
2	18.1		61.0	57.9	55.4	53.7	46.9	42.7	44.1	42.9	42.3	40.5	2
3	40.4	41.0		70.5	59.3	56.4	46.7	48.5	48.1	48.6	46.5	43.5	3
4	43.9	44.3	28.0		56.3	55.4	46.5	47.0	45.1	47.2	47.4	42.3	4
5	40.7	42.3	45.0	45.0		68.0	54.0	46.8	46.6	46.4	49.0	47.2	5
6	45.8	48.9	46.0	47.3	32.4		53.6	48.6	48.2	48.6	49.0	49.2	6
7	74.1	71.0	69.4	67.3	64.3	64.5		49.8	49.2	49.8	47.7	48.2	7
8	68.1	66.2	63.4	63.1	65.5	64.2	56.1		97.7	99.7	48.4	45.8	8
9	67.0	65.4	63.7	64.6	64.6	64.1	56.6	1.1		95.9	47.6	44.8	9
10	67.2	65.2	61.8	61.4	64.1	63.0	56.3	0.2	1.1		48.4	45.3	10
11	88.6	85.8	81.0	77.0	77.4	82.4	83.1	71.1	71.1	69.9		48.3	11
12	95.7	90.4	95.4	91.5	84.5	82.8	91.9	73.4	73.8	73.3	59.9		12
	1	2	3	4	5	6	7	8	9	10	11	12	

ARAFAE1 U29142

BNAFAE1 U50771

EL2

EL3

EL5

EL7

EL6

JOJOKCS U37088

JOKCS10 I14084

JOKCS11 I14085

EL1

EL4

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Example 4

Expression of EL1 and EL2 in Yeast

The open reading frames (ORFs) for the EL2, EL4 and EL7 clones were amplified by PCR. The EL2 ORF was cloned into λ YES using the primers: CTCGAGCAAGTCCACTACCACGCA and CTCGAGCGAGTCAGAAGGAACAAA. The EL4 ORF was cloned into pYEUra3 using the primers: GATAATTTAGAGAGGCACAGGGT and GTCGACACAAGAATGGGTAGATCCAA. The EL7 ORF was cloned into pYEUra3 using the primers: CAGTTCCTCAAACGAAGCTA and GTCGACTTCTCAATGGACGGTGCCGGA. Amplified products were cloned into pYEUra3 under the control of, and 3' to, the GAL1 promoter. The resulting plasmids were transformed into yeast as described in Example 1.

Yeast cultures containing full-length EL1 in λ YES and full-length EL2 in pYEUra3 were grown in the presence of galactose or glucose as described in Example 2. Microsomes were then prepared from each of the cultures and fatty acid elongation assays were carried out as described in Example 2.

In the first experiment, microsomes were prepared from galactose-induced cultures of EL1, EL2 and FAE1, and incubated with either [1- 14 C] 18:0 acyl-CoA or [1- 14 C] 18:1 acyl-CoA as substrate. The amounts of various reaction products synthesized after 30 minutes (min) were determined as described in Example 2. The results when 18:0 acyl-CoA was the substrate are shown in Table 3. The results when 18:1 acyl-CoA was the substrate are shown in Table 4.

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Table 3.
Elongation of 18:0-CoA by FAE1, EL1 and EL2 Genes
Expressed in Yeast

Acyl-CoA Product	β-Keto Acyl Synthase Gene					
	FAE1		EL1		EL2	
	Rate ¹	(%)	Rate	(%)	Rate	(%)
20:0	0.369	64.3	0.084	38.8	0.108	41.8
22:0	0.113	18.6	0.047	21.9	0.053	20.7
24:0	0.065	10.7	0.043	19.9	0.052	20.3
26:0	0.038	6.3	0.042	19.4	0.044	17.2
Total	0.585	100.0	0.216	100.0	0.258	100.0

¹ Nanomoles/minute/mg of microsomal protein

Table 4.
Elongation of 18:1-CoA by FAE1, EL1 and EL2 Genes
Expressed in Yeast

Acyl-CoA Product	β-Keto Acyl Synthase Gene					
	FAE1		EL1		EL2	
	Rate ¹	(%)	Rate	(%)	Rate	(%)
20:1	1.131	84.6	0.111	80.8	0.091	84.1
22:1	0.206	15.4	0.026	19.2	0.017	15.9
24:1	0.0	0.0	0.0	0.0	0.0	0.0
26:1	0.0	0.0	0.0	0.0	0.0	0.0
Total	1.337	100.0	0.137	100.0	0.108	100.0

¹ Nanomoles/minute/mg of microsomal protein

The results shown in Tables 3 and 4 indicate that the EL1 and EL2 gene products have β-ketoacyl synthase (KAS) activity and that the KAS reaction product can be utilized to form VLCFAs. The specific activities of the 3 KAS enzymes cannot be compared, since the relative amount of the heterologous KAS protein in each microsomal preparation is not known. However, the proportions of various reaction products can be compared between FAE1, EL1 and EL2.

The data shown in Table 3 indicate that the EL1 and EL2 KAS activities result in a higher proportion of saturated VLCFAs than does the FAE1 KAS activity. These

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results suggest that EL1 and EL2 encode novel gene products, because EL1 and EL2 have a greater preference for C22:0 and C24:0 acyl-CoA substrates than does FAE1.

A comparison of the relative elongation activity of FAE1 with 18:0 and 18:1 substrates (Tables 3 and 4) indicates that FAE1 is more active when 18:1 is the substrate than when 18:0 is the substrate. In contrast, the overall rate of product formation with EL1 is less when 18:1 is the substrate than when 18:0 is the substrate (Tables 3 and 4). EL2 is also less active when 18:1 is the substrate than when 18:0 is the substrate (Tables 3 and 4). These results support the conclusion that EL1 and EL2 encode novel gene products and suggest that EL1 and EL2 have a preference for saturated fatty acids as substrates, whereas the FAE1 gene product has a preference for monounsaturated fatty acids as substrates.

In a second experiment, microsomes were prepared from galactose-induced and from glucose-repressed yeast cultures containing EL1 or EL2 coding sequences. The microsomal preparations were incubated with either 18:0 acyl-CoA or 18:1 acyl-CoA as substrate and the fatty acid reaction products determined as described above. The results with the 18:0 substrate are shown in Table 5. The results with the 18:1 substrate are shown in Table 6.

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Table 5.
Elongation of 18:0-CoA by EL1 and EL2
With and Without Induction of Gene Expression

Acyl CoA	8-Keto Acyl Synthase Gene							
	EL1				EL2			
	+Glucose		+Galactose		+Glucose		+Galactose	
	Rate ¹	(%)	Rate	(%)	Rate	(%)	Rate	(%)
20:0	0.007	100.0	0.074	55.8	0.030	81.3	0.107	43.1
22:0	0.000	0.0	0.023	17.4	0.002	5.1	0.044	17.8
24:0	0.000	0.0	0.020	15.3	0.005	13.6	0.048	19.1
26:0	0.000	0.0	0.015	11.5	0.000	0.0	0.050	20.0
Total	0.007	100.0	0.133	100.0	0.037	100.0	0.249	100.0

¹ Nanomoles/minute/mg of microsomal protein

Table 6.
Elongation of 18:1-CoA by EL1 and EL2
With and Without Induction of Gene Expression

Acyl CoA	8-Keto Acyl Synthase Gene							
	EL1				EL2			
	+Glucose		+Galactose		+Glucose		+Galactose	
	Rate ¹	(%)	Rate	(%)	Rate	(%)	Rate	(%)
20:1	0.062	100.0	0.081	100.0	0.043	100.0	0.089	100.0
22:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
24:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
26:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
Total	0.062	100.0	0.081	100.0	0.043	100.0	0.089	100.0

¹ Nanomoles/minute/mg of microsomal protein

The results in Table 5 show *in vitro* elongase activity for EL1 and EL2 under induced (galactose) and uninduced (glucose) conditions. The comparison indicates that induction with galactose results in a large increase in overall elongase activity when 18:0 acyl CoA is the substrate (about 19-fold and 7-fold for EL1 and EL2, respectively). In contrast, induction when 18:1 acyl CoA is the substrate results in only a small increase in elongase activity (about 1.3-fold and 2-fold for EL1 and EL2, respectively), as shown in Table 6.

The results in Table 5 show that little or no VLCFA products are made by yeast microsomes under uninduced conditions. Upon induction of EL1 and EL2 gene

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expression, however, significant quantities of C20:0, C22:0, C24:0 and C26:0 are made. The data in Tables 5 and 6 are consistent with the results in Tables 3 and 4, which indicated that EL1 and EL2 were more active with a saturated fatty acid substrate than with a monounsaturated substrate.

The data in Tables 5 and 6 are also consistent with the data in Tables 3 and 4 indicating that the EL1 and EL2 gene products are more active in converting C24:0 to C26:0 than is FAE1.

In a third experiment, microsomes from induced and uninduced cultures containing EL1 or EL2 were incubated in the absence of cofactors involved in the β -ketoacyl condensation reaction. Cultures were induced and microsomes were prepared as described in Example 2. In vitro assays were carried out as described in Example 2, except that either ATP, CoASH or both were omitted from the enzyme reaction mixture. In addition, one reaction was carried out in a complete mixture having 0.01 mM of cerulenin (Sigma, St. Louis, MO). Cerulenin is an inhibitor of some condensing enzymes. The results are shown in Tables 7-9.

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Table 7.
Effect of Cofactors on 18:0-CoA Elongation¹

Gene	Expt ⁴	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+ Cer ³
EL1	1	.037	.109	.095	.105	.119	.141
	2	N.D.	.090	.125	.093	.270	.176
EL2	1	.033	.112	.168	.127	.143	.238
	2	N.D.	.120	.178	.133	.195	.302

¹ Activity in nanomoles/minute/mg of microsomal protein.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

⁴ Experiment No.

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Table 8.
Effect of Cofactors on Elongation Products of EL1¹

Prod.	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+Cer ³
20:0	53.9	46.2	34.4	47.8	41.7	46.7
22:0	14.4	18.7	13.7	18.0	19.4	16.2
24:0	18.5	18.1	20.6	19.1	16.7	17.7
26:0	13.2	17.1	31.4	15.2	22.3	19.4
Total	100.0	100.0	100.0	100.0	100.0	100.0

¹ Amount of indicated product as a percent of total products formed. Results of one experiment for +Glucose; Average of two experiments for other conditions.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

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Table 9.
Effect of Cofactors on Elongation Products of EL2¹

Prod.	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+Cer ³
20:0	54.5	47.1	34.1	45.3	38.0	41.8
22:0	17.1	19.1	16.4	19.2	15.9	16.1
24:0	5.8	19.4	20.8	19.9	18.4	20.4
26:0	22.6	14.5	28.9	15.8	27.8	21.8
Total	100.0	100.0	100.0	100.0	100.0	100.0

¹ Amount of indicated product as a percent of total products formed. Results of one experiment for +Glucose; Average of two experiments for other conditions.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

The results in Table 7 indicate that omission of ATP and/or CoA from the incubation mixture does not have a significant effect on the overall amounts of VLCFAs synthesized by the *in vitro* KAS activity of EL1 or EL2. The results also show that cerulenin does not inhibit the KAS activity of EL1 or EL2. The data in Table 8 and 9 confirm that EL1 and EL2 KAS activity produces significant amounts of C24:0 and C26:0 acyl CoA products.

To the extent not already indicated, it will be understood by those of ordinary skill in the art that any one of the various specific embodiments herein described and illustrated may be further modified to incorporate features shown in other of the specific embodiments.

The foregoing detailed description has been provided for a better understanding of the invention only and no unnecessary limitation should be understood therefrom as some modifications will be apparent to those

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skilled in the art without deviating from the spirit and scope of the appended claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: CARGILL, INCORPORATED
- (ii) TITLE OF THE INVENTION: FATTY ACID ELONGASES
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
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 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/868,373
 - (B) FILING DATE: 03-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lundquist, Ronald C
 - (B) REGISTRATION NUMBER: 37,875
 - (C) REFERENCE/DOCKET NUMBER: 07039/064WO1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-335-5050
 - (B) TELEFAX: 612-288-9696
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGATCGAG	AGAGATTAAC	GGCGGAGATG	GCGTTTCGAG	ATTCATCATC	GGCCGTTTATA	60
AGAATTTCGAA	GACGTTTGCC	GGATTTATTA	ACGTCCGTTA	AGCTCAAATA	CGTGAAGCTT	120
GGACTTCACA	ACTCTTGCAA	CGTGACCACC	ATTCTCTTCT	TCTTAATTAT	TCTTCCTTTA	180
ACCGGAACCG	TGCTGGTTCA	GCTAACCCGT	CTAACGTTTC	ATACGTTCTC	TGAGCTTTGG	240
TCTAACCCAGG	CGGTTCAACT	CGACACGGCG	ACGAGACTTA	CCTGCTTGGT	TTTCCTCTCC	300
TTCGTTTTGA	CCCTCTACGT	GGCTAACCCG	TCTAAACCCG	TTTACCTAGT	GGATTTCTCC	360
TGCTACAAAC	CGGAAGACGA	GCGTAAAATA	TCAGTAGATT	CGTTCTTGAC	GATGACTGAG	420
GAAAATGGAT	CATTCACCGA	TGACACGGTT	CAGTTCAGC	AAAGAATCTC	GAACCGGGCC	480

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GGTTTGGGAG ACGAGACGTA TCTGCCACGT GGCATAACTT CAACGCCCCC GAAGCTAAAT 540
ATGTCAGAGG CACGTGCCGA AGCTGAAGCC GTTATGTTTG GAGCCTTAGA TTCCCTCTTC 600
GAGAAAACCG GAATTAAACC GGCCGAAGTC GGAATCTTGA TAGTAAACTG CAGCTTATTC 660
AATCCGACGC CGTCTCTATC AGCGATGATC GTGAACCAAT ACAAGATGAG AGAAGACATC 720
AAAAGTTACA ACCTCGGAGG AATGGGTTGC TCCGCCGGAT TAATCTCAAT CGATCTCGCT 780
AACAATCTCC TCAAAGCAAA CCCTAATTCT TACGCTGTCTG TGGTAAGCAC GGAAAACATA 840
ACCCTAAACT GGTACTTCGG AAATGACCGG TCAATGCTCC TCTGCAACTG CATCTTCCGA 900
ATGGGCGGAG CTGCGATTCT CCTCTCTAAC CGCCGTCAAG ACCGGAAGAA GTCAAAGTAC 960
TCGCTGGTCA ACGTCGTTCT AACACATAAA GGATCAGACG ACAAGAACTA CAATTGCGTG 1020
TACCAGAAGG AAGACGAGAG AGGAACAATC GGTGTCTCTT TAGCTAGAGA GCTCATGTCT 1080
GTCGCCGGAG ACGCTCTGAA AACAAACATC ACGACTTTAG GACCGATGGT TCTTCCATTG 1140
TCAGAGCAGT TGATGTTCTT GATTTCCTTG GTCAAAAGGA AGATGTTCAA GTTAAAGTT 1200
AAACCGTATA TTCCGGATTT CAAGCTAGCT TTCGAGCATT TCTGTATTCA CGCAGGAGGT 1260
AGAGCGGTTT TAGACGAAGT GCAGAAGAAT CTTGATCTCA AAGATTGGCA CATGGAACCT 1320
TCTAGAATGA CTTTGCACAG ATTTGGTAAC ACTTCGAGTA GCTCGCTTTG GTATGAGATG 1380
GCTTATACCG AAGCTAAGGG TCGGGTTAAA GCTGGTGACC GACTTTGGCA GATTGCGTTT 1440
GGATCGGGTT TCAAGTGTAA TAGTGCGGTT TGGAAAGCGT TACGACCGGT TTCGACGGAG 1500
GAGATGACCG GTAATGCTTG GGCTGGTTCTG ATTGATCAAT ATCCGGTTAA AGTTGTGCAA 1560

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Asp Arg Glu Arg Leu Thr Ala Glu Met Ala Phe Arg Asp Ser Ser
 1           5           10           15
Ser Ala Val Ile Arg Ile Arg Arg Arg Leu Pro Asp Leu Leu Thr Ser
          20          25          30
Val Lys Leu Lys Tyr Val Lys Leu Gly Leu His Asn Ser Cys Asn Val
          35          40          45
Thr Thr Ile Leu Phe Phe Leu Ile Ile Leu Pro Leu Thr Gly Thr Val
 50          55          60
Leu Val Gln Leu Thr Gly Leu Thr Phe Asp Thr Phe Ser Glu Leu Trp
65          70          75          80
Ser Asn Gln Ala Val Gln Leu Asp Thr Ala Thr Arg Leu Thr Cys Leu
          85          90          95
Val Phe Leu Ser Phe Val Leu Thr Leu Tyr Val Ala Asn Arg Ser Lys
          100         105         110
Pro Val Tyr Leu Val Asp Phe Ser Cys Tyr Lys Pro Glu Asp Glu Arg
          115         120         125
Lys Ile Ser Val Asp Ser Phe Leu Thr Met Thr Glu Glu Asn Gly Ser
130         135         140
Phe Thr Asp Asp Thr Val Gln Phe Gln Gln Arg Ile Ser Asn Arg Ala
145         150         155         160
Gly Leu Gly Asp Glu Thr Tyr Leu Pro Arg Gly Ile Thr Ser Thr Pro
          165         170         175
Pro Lys Leu Asn Met Ser Glu Ala Arg Ala Glu Ala Glu Val Met
          180         185         190
Phe Gly Ala Leu Asp Ser Leu Phe Glu Lys Thr Gly Ile Lys Pro Ala
          195         200         205
Glu Val Gly Ile Leu Ile Val Asn Cys Ser Leu Phe Asn Pro Thr Pro
210         215         220
Ser Leu Ser Ala Met Ile Val Asn His Tyr Lys Met Arg Glu Asp Ile
225         230         235         240
Lys Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser
          245         250         255
Ile Asp Leu Ala Asn Asn Leu Leu Lys Ala Asn Pro Asn Ser Tyr Ala
          260         265         270
Val Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Phe Gly Asn
          275         280         285

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Asp Arg Ser Met Leu Leu Cys Asn Cys Ile Phe Arg Met Gly Gly Ala
 290 295 300
 Ala Ile Leu Leu Ser Asn Arg Arg Gln Asp Arg Lys Lys Ser Lys Tyr
 305 310 315 320
 Ser Leu Val Asn Val Arg Thr His Lys Gly Ser Asp Asp Lys Asn
 325 330 335
 Tyr Asn Cys Val Tyr Gln Lys Glu Asp Glu Arg Gly Thr Ile Gly Val
 340 345 350
 Ser Leu Ala Arg Glu Leu Met Ser Val Ala Gly Asp Ala Leu Lys Thr
 355 360 365
 Asn Ile Thr Thr Leu Gly Pro Met Val Leu Pro Leu Ser Glu Gln Leu
 370 375 380
 Met Phe Leu Ile Ser Leu Val Lys Arg Lys Met Phe Lys Leu Lys Val
 385 390 395 400
 Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys Ile
 405 410 415
 His Ala Gly Gly Arg Ala Val Leu Asp Glu Val Gln Lys Asn Leu Asp
 420 425 430
 Leu Lys Asp Trp His Met Glu Pro Ser Arg Met Thr Leu His Arg Phe
 435 440 445
 Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Met Ala Tyr Thr Glu
 450 455 460
 Ala Lys Gly Arg Val Lys Ala Gly Asp Arg Leu Trp Gln Ile Ala Phe
 465 470 475 480
 Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg Pro
 485 490 495
 Val Ser Thr Glu Glu Met Thr Gly Asn Ala Trp Ala Gly Ser Ile Asp
 500 505 510
 Gln Tyr Pro Val Lys Val Val Gln
 515 520

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTACC	CCATGAAGAA	GGTAAAAATC	TTTTTCAACT	ACCTCATGGC	GCATCGCTTC	60
AAGCTCTGCT	TCATTACCATT	AATGGTTGCT	ATAGCCGTGG	AGGCGTCTCG	TCTTTCCACA	120
CAAGATCTCC	AAAACTTTTA	CCTCTACTTA	CAAAACAACC	ACACATCTCT	AACCATGTTT	180
TTCCTTTACC	TCGCTCTCGG	GTCGACTCTT	TACCTCATGA	CCCGGCCCAA	ACCCGTTTAT	240
CTCGTTGACT	TTAGCTGCTA	CCTCCCACCG	TCCGATCTCA	AAGCCAGCAC	CCAGAGGATC	300
ATGCAACACG	TAAGGCTTGT	ACGAGAAGCA	GGCGCGTGGA	AGCAAGAGTC	CGATTACTTG	360
ATGGACTTCT	GCGAGAAGAT	TCTAGAACGT	TCCGGTCTAG	GCCAAGAGAC	GTACGTACCC	420
GAAGGTCTTC	AAACTTTGCC	ACTACAACAG	AATTTGGCTG	TATCACGTAT	AGAGACGGAG	480
GAAGTTATTA	TTGGTGCGGT	CGATAATCTG	TTTCGCAACA	CGGGAATAAG	CCCTAGTGAT	540
ATAGGTATAT	TGGTGGTGAA	TTCAAGCACT	TTTAATCCAA	CACCTTCGCT	ATCAAGTATC	600
TTAGTGAATA	AGTTTAAACT	TAGGGATAAT	ATAAAGAGCT	TGAATCTTGG	TGGGATGGGG	660
TGTAGCGCTG	GAGTCATCGC	TATCGATGCG	GCTAAGAGCT	TGTTACAAGT	TCATAGAAAC	720
ACTTATGCTC	TTGTGGTGAG	CACGGAGAAC	ATCACTCAAA	ACTTGTACAT	GGGTAACAAC	780
AAATCAATGT	TGGTTACAAA	CTGTTTGTTT	CGTATAGGTG	GGGCCGCGAT	TTTGCTTTCT	840
AACCGGTCTA	TAGATCGTAA	ACGCGCAAAA	TACGAGCTTG	TTACACCCGT	GCGGGTCCAT	900
ACCGGAGCAG	ATGACCGATC	CTATGAATGT	GCAACTCAAG	AAGAGGATGA	AGATGGCATA	960
GTTGGGGTTT	CCTTGTCAAA	GAATCTACCA	ATGGTAGCTG	CAAGAACCCT	AAAGATCAAT	1020
ATCGCAACTT	TGGGTCCGCT	TGTTCTTCCC	ATAAGCGAGA	AGTTTCACCT	CTTTGTGAGG	1080
TTCGTTAAAA	AGAAGTTTCT	CAACCCCAAG	CTAAAGCATT	ACATTCCGGA	TTTCAAGCTC	1140
GCATTCGAGC	ATTTCTGTAT	CCATGCGGGT	GGTAGAGCGC	TAATTGATGA	GATGGAGAAG	1200
AATCTTCATC	TAACTCCACT	AGACGTTGAG	GCTTCAAGAA	TGACATTACA	CAGGTTTGGT	1260
AATACCTCTT	CGAGCTCCAT	TTGGTACGAG	TTGGCTTACA	CAGAAGCCAA	AGGAAGGATG	1320
ACGAAAGGAG	ATAGGATTTG	GCAGATTGCG	TTGGGGTCAG	GTTTTAAGTG	TAATAGTTCA	1380

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GTTTGGGTGG CTCTTCGTAA CGTCAAGCCT TCTACTAATA ATCCTTGGGA ACAGTGTCTA 1440
 CACAAATATC CAGTTGAGAT CGATATAGAT TTAAAAGAG 1479

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Tyr	Pro	Met	Lys	Lys	Val	Lys	Ile	Phe	Phe	Asn	Tyr	Leu	Met
1				5				10					15		
Ala	His	Arg	Phe	Lys	Leu	Cys	Phe	Leu	Pro	Leu	Met	Val	Ala	Ile	Ala
			20					25				30			
Val	Glu	Ala	Ser	Arg	Leu	Ser	Thr	Gln	Asp	Leu	Gln	Asn	Phe	Tyr	Leu
			35				40					45			
Tyr	Leu	Gln	Asn	Asn	His	Thr	Ser	Leu	Thr	Met	Phe	Phe	Leu	Tyr	Leu
	50				55					60					
Ala	Leu	Gly	Ser	Thr	Leu	Tyr	Leu	Met	Thr	Arg	Pro	Lys	Pro	Val	Tyr
65					70					75					80
Leu	Val	Asp	Phe	Ser	Cys	Tyr	Leu	Pro	Pro	Ser	His	Leu	Lys	Ala	Ser
				85					90					95	
Thr	Gln	Arg	Ile	Met	Gln	His	Val	Arg	Leu	Val	Arg	Glu	Ala	Gly	Ala
			100					105					110		
Trp	Lys	Gln	Glu	Ser	Asp	Tyr	Leu	Met	Asp	Phe	Cys	Glu	Lys	Ile	Leu
		115					120					125			
Glu	Arg	Ser	Gly	Leu	Gly	Gln	Glu	Thr	Tyr	Val	Pro	Glu	Gly	Leu	Gln
	130					135					140				
Thr	Leu	Pro	Leu	Gln	Gln	Asn	Leu	Ala	Val	Ser	Arg	Ile	Glu	Thr	Glu
145					150					155					160
Glu	Val	Ile	Ile	Gly	Ala	Val	Asp	Asn	Leu	Phe	Arg	Asn	Thr	Gly	Ile
				165					170					175	
Ser	Pro	Ser	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Thr	Phe	Asn
			180					185					190		
Pro	Thr	Pro	Ser	Leu	Ser	Ser	Ile	Leu	Val	Asn	Lys	Phe	Lys	Leu	Arg
		195					200					205			
Asp	Asn	Ile	Lys	Ser	Leu	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly
	210					215					220				
Val	Ile	Ala	Ile	Asp	Ala	Ala	Lys	Ser	Leu	Leu	Gln	Val	His	Arg	Asn
225					230					235					240
Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn	Leu	Tyr
				245					250					255	
Met	Gly	Asn	Asn	Lys	Ser	Met	Leu	Val	Thr	Asn	Cys	Leu	Phe	Arg	Ile
			260					265					270		
Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Arg	Ser	Ile	Asp	Arg	Lys	Arg
		275					280					285			
Ala	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Val	His	Thr	Gly	Ala	Asp
	290					295					300				
Asp	Arg	Ser	Tyr	Glu	Cys	Ala	Thr	Gln	Glu	Glu	Asp	Glu	Asp	Gly	Ile
305					310					315					320
Val	Gly	Val	Ser	Leu	Ser	Lys	Asn	Leu	Pro	Met	Val	Ala	Ala	Arg	Thr
				325					330					335	
Leu	Lys	Ile	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Ile	Ser
			340					345					350		
Glu	Lys	Phe	His	Phe	Phe	Val	Arg	Phe	Val	Lys	Lys	Lys	Phe	Leu	Asn
		355					360					365			
Pro	Lys	Leu	Lys	His	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Glu	His
	370					375						380			
Phe	Cys	Ile	His	Ala	Gly	Arg	Ala	Leu	Ile	Asp	Glu	Met	Glu	Lys	
385					390					395				400	
Asn	Leu	His	Leu	Thr	Pro	Leu	Asp	Val	Glu	Ala	Ser	Arg	Met	Thr	Leu
				405					410					415	

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(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 1512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(2) INFORMATION FOR SEO ID NO:6:

(A) LENGTH: 504 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Arg Gln Gly Arg Thr Lys Ser Lys His Leu Ser Lys Thr Ile Cys
1 5 10 15
Pro Thr Leu Arg Leu Ser Pro Met Lys Asn Leu Lys Met Val Phe Phe
20 25 30

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Lys Ile Leu Phe Ile Ser Leu Met Ala Gly Leu Ala Met Lys Gly Ser
 35 40 45
 Lys Ile Asn Val Glu Asp Leu Gln Lys Phe Ser Leu His His Thr Gln
 50 55 60
 Asn Asn Leu Gln Thr Ile Ser Leu Leu Leu Phe Leu Val Val Phe Val
 65 70 75 80
 Trp Ile Leu Tyr Met Leu Thr Arg Pro Lys Pro Val Tyr Leu Val Asp
 85 90 95
 Phe Ser Cys Tyr Leu Pro Pro Ser His Leu Lys Val Ser Ile Gln Thr
 100 105 110
 Leu Met Gly His Ala Arg Arg Ala Arg Glu Ala Gly Met Cys Trp Lys
 115 120 125
 Asn Lys Glu Ser Asp His Leu Val Asp Phe Gln Glu Lys Ile Leu Glu
 130 135 140
 Arg Ser Gly Leu Gly Gln Glu Thr Tyr Ile Pro Glu Gly Leu Gln Cys
 145 150 155 160
 Phe Pro Leu Gln Gln Gly Met Gly Ala Ser Arg Lys Glu Thr Glu Glu
 165 170 175
 Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Arg Asn Thr Gly Val Lys
 180 185 190
 Pro Asp Asp Ile Gly Ile Leu Val Val Asn Ser Ser Thr Phe Asn Pro
 195 200 205
 Thr Pro Ser Leu Ala Ser Met Ile Val Asn Lys Tyr Lys Leu Arg Asp
 210 215 220
 Asn Ile Lys Ser Leu Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val
 225 230 235 240
 Ile Ala Val Asp Val Ala Lys Gly Leu Leu Gln Val His Arg Asn Thr
 245 250 255
 Tyr Ala Ile Val Val Ser Thr Glu Asn Ile Thr Gln Asn Leu Tyr Leu
 260 265 270
 Gly Lys Asn Lys Ser Met Leu Val Thr Asn Cys Leu Phe Arg Val Gly
 275 280 285
 Gly Ala Ala Val Leu Leu Ser Asn Arg Ser Arg Asp Arg Asn Arg Ala
 290 295 300
 Lys Tyr Glu Leu Val His Thr Val Arg Ile His Thr Gly Ser Asp Asp
 305 310 315 320
 Arg Ser Phe Glu Cys Ala Thr Gln Glu Glu Asp Glu Asp Gly Ile Ile
 325 330 335
 Gly Val Thr Leu Thr Lys Asn Leu Pro Met Val Ala Ala Arg Thr Leu
 340 345 350
 Lys Ile Asn Ile Ala Thr Leu Gly Pro Leu Val Leu Pro Leu Lys Glu
 355 360 365
 Lys Leu Ala Phe Phe Ile Thr Phe Val Lys Lys Lys Tyr Phe Lys Pro
 370 375 380
 Glu Leu Arg Asn Tyr Thr Pro Asp Phe Lys Leu Ala Phe Glu His Phe
 385 390 395 400
 Cys Ile His Ala Gly Gly Arg Ala Leu Ile Asp Glu Leu Glu Lys Asn
 405 410 415
 Leu Lys Leu Ser Pro Leu His Val Glu Ala Ser Arg Met Thr Leu His
 420 425 430
 Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr
 435 440 445
 Thr Glu Ala Lys Gly Arg Met Lys Glu Gly Asp Arg Ile Trp Gln Ile
 450 455 460
 Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ser Val Trp Val Ala Leu
 465 470 475 480
 Arg Asp Val Lys Pro Ser Ala Asn Ser Pro Trp Glu Asp Cys Met Asp
 485 490 495
 Arg Tyr Pro Val Glu Ile Asp Ile
 500

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

ATGGGTTAGAT CCAACGAGCA AGATCTGCTC TCTACCGAGA TCGTTAATCG TGGGATCGAA      60
CCATCCGGTC CTAACGCCGG CTCACCAACG TTCTCGGTTA GGGTCAGGAG ACGTTTGCCT      120
GATTTTCTTC AGTCGGTGAA CTTGAAGTAC GTGAAACTTG GTTACCACTA CCTCATAAAC      180
CATGCGGTTT ATTTGGCGAC CATACCGGTT CTGTGCTGG TTTTGTAGTC TGAGGTTGGG      240
AGTTTAAGCA GAGAAGAGAT TTGGAAGAAG CTTTGGGACT ATGATCTTGC AACTGTTATC      300
GGATTCTTCG GTGTCTTTGT TTTAACCGCT TGTGTCTACT TCATGTCTCG TCCTCGCTCT      360
GTTTATCTTA TTGATTTTCG TTGTTACAAG CCTCCGATG AACACAAGGT GACAAAAGAA      420
GAGTTCATAG AACTAGCGAG AAAATCAGGG AAGTTCGACG AAGAGACACT CGGTTTCAAG      480
AAGAGGATCT TACAAGCCTC AGGCATAGGC GACGAGACAT ACGTCCCAAG ATCCATCTCT      540
TCATCAGAAA ACATAACAAC GATGAAAGAA GGTTCGTGAAG AAGCCTCTAC AGTGATCTTT      600
GGAGCACTAG ACGAACTCTT CGAGAAGACA CGGTGTAAGC CTAAAGACGT TGGTGTCTCT      660
GTGGTTAACT GTAGCATTTT CAACCCGACA CCGTCGTTGT CCGCAATGGT GATAAACCAT      720
TACAAGATGA GAGGGAACAT ACTTAGTTAC AACCTTGGAG GGATGGGATG TTCGGCTGGA      780
ATCATAGCTA TTGATCTTGC TCGTGACATG CTTCAGTCTA ACCCTAATAG TTATGCTGTT      840
GTTGTGAGTA CTGAGATGGT TGGGTATAAT TGGTACGTGG GAAGTGACAA GTCAATGGTT      900
ATACCTAATT GTTCTTTAG GATGGGTTGT TCTGCCGTTA TGCTCTCTAA CCGTCGTCGT      960
GACTTTCGCC ATGCTAAGTA CCGTCTCGAG CACATTGTCC GAACTCATAA GGCTGCTGAC      1020
GACCGTAGCT TCAGGAGTGT GTACCAGGAA GAAGATGAAC AAGGATTCAA GGGGTGAAG      1080
ATAAGTAGAG ACTTAATGGA AGTTGGAGGT GAAGCTCTCA AGACAAACAT CACTACCTTA      1140
GGTCTCTTGT TCCTACCTTT CTCCGAGCAG CTCTCTTCT TTGCTGCTTT GGTCCGCCGA      1200
ACATTCTCAC CTGCTGCCAA AACGTCACA ACCACTTCTT TCTCTACTTC CGCCACCGCA      1260
AAAACCAATG GAATCAAGTC TTCCTCTTCC GATCTGTCCA AGCCATACAT CCCGACTAC      1320
AAGCTCGCCT TCGAGCATTT TTGCTTCCAC GCGGCAAGCA AAGTAGTGCT TGAAGAGCTT      1380
CAAAAGAATC TAGGCTTGAG TGAAGAGAAT ATGGAGGCTT CTAGGATGAC ACTTCACAGG      1440
TTTGGAACA CTTCTAGCAG TGAATCTGG TATGAGTTGG CTTACATGGA GGCCAAGGAA      1500
AGTGTTCGTA GAGGCGATAG GGTTTGGCAG ATCGCTTTCG GTTCTGGTTT TAAGTGTAA      1560
AGTGTGGTGT GGAAGGCAAT GAGGAAGGTG AAGAAGCCAA CCAGGAACAA TCCTTGGGTG      1620
GATTGCATCA ACCGTTACCC TGTGCCTCTC

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Gly Arg Ser Asn Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn
 1           5           10           15
Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser
          20          25          30
Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu
          35          40          45
Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr
          50          55          60
Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly
          65          70          75          80
Ser Leu Ser Arg Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu
          85          90          95
Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val
          100          105          110

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Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys
 115 120 125
 Tyr Lys Pro Ser Asp Glu His Lys Val Thr Lys Glu Phe Ile Glu
 130 135 140
 Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Thr Leu Gly Phe Lys
 145 150 155 160
 Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro
 165 170 175
 Arg Ser Ile Ser Ser Ser Glu Asn Ile Thr Thr Met Lys Glu Gly Arg
 180 185 190
 Glu Glu Ala Ser Thr Val Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu
 195 200 205
 Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn Cys
 210 215 220
 Ser Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn His
 225 230 235 240
 Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly
 245 250 255
 Cys Ser Ala Gly Ile Ile Ala Ile Asp Leu Ala Arg Asp Met Leu Gln
 260 265 270
 Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly
 275 280 285
 Tyr Asn Trp Tyr Val Gly Ser Asp Lys Ser Met Val Ile Pro Asn Cys
 290 295 300
 Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg Arg
 305 310 315 320
 Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr His
 325 330 335
 Lys Ala Ala Asp Asp Arg Ser Phe Arg Ser Val Tyr Gln Glu Glu Asp
 340 345 350
 Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu Val
 355 360 365
 Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val
 370 375 380
 Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Val Arg Arg
 385 390 395 400
 Thr Phe Ser Pro Ala Ala Lys Thr Ser Thr Thr Thr Ser Phe Ser Thr
 405 410 415
 Ser Ala Thr Ala Lys Thr Asn Gly Ile Lys Ser Ser Ser Ser Asp Leu
 420 425 430
 Ser Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys
 435 440 445
 Phe His Ala Ala Ser Lys Val Val Leu Glu Glu Leu Gln Lys Asn Leu
 450 455 460
 Gly Leu Ser Glu Glu Asn Met Glu Ala Ser Arg Met Thr Leu His Arg
 465 470 475 480
 Phe Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met
 485 490 495
 Glu Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala
 500 505 510
 Phe Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg
 515 520 525
 Lys Val Lys Lys Pro Thr Arg Asn Asn Pro Trp Val Asp Cys Ile Asn
 530 535 540
 Arg Tyr Pro Val Pro Leu
 545 550

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCGAGCTACG	TCAGGGCTTT	TATATGCACA	AATTCTCATA	AAGTTTTCAA	TTTTATTCCA	60
TTTTTCTCGG	AAGCCATGGA	AGCTGCTAAT	GAGCCTGTTA	ATGGCGGATC	CGTACAGATC	120
CGAACAGAGA	ACAACGAAAG	ACGAAAGCTT	CCTAATTTCT	TACAAAGCGT	CAACATGAAA	180
TACGTCAAGC	TAGGTTATCA	TTACCTCATT	ACTCATCTCT	TCAAGCTCTG	TTTGGTTCCA	240
TTAATGGCGG	TTTTAGTCAC	AGAGATCTCT	CGATTAACAA	CAGACGATCT	TTACCAGATT	300
TGGCTTCATC	TCCAATACAA	TCTCGTTGCT	TTCATCTTTC	TCTCTGCTTT	AGCTATCTTT	360
GGCTCCACCG	TTTACATCAT	GAGTCGTCCC	AGATCTGTTT	ATCTCGTTGA	TTACTCTTGT	420
TATCTTCCTC	CGGAGAGTCT	TCAGGTTAAG	TATCAGAAGT	TTATGGATCA	TTCTAAGTTG	480
ATTGAAGATT	TCAATGAGTC	ATCTTTAGAG	TTTCAGAGGA	AGATTCTTGA	ACGTTCTGGT	540
TTAGGAGAAG	AGACTTATCT	CCCTGAAGCT	TTACATTGTA	TCCCTCCGAG	GCCTACGATG	600
ATGGCGGCTC	GTGAGGAATC	TGAGCAGGTA	ATGTTTGGTG	CTCTTGATAA	GCTTTTCGAG	660
AATACCAAGA	TTAACCCTAG	GGATATTGGT	GTGTTGGTTG	TGAATTGTAG	CTTGTTTAAT	720
CCTACACCTT	CGTTGTCAGC	TATGATTGTT	AACAAGTATA	AGCTTAGAGG	GAATGTTAAG	780
AGTTTAAACC	TTGGTGGAAT	GGGGTGTAAGT	GCTGGTGTTA	TCTCTATCGA	TTTAGCTAAA	840
GATATGTTGC	AAGTTCATAG	GAATACTTAT	GCTGTTGTGG	TTAGTACTGA	GAACATTACT	900
CAGAATTGGT	ATTTTGGGAA	TAAGAAGGCT	ATGTTGATTC	CGAATTGTTT	GTTTCGTGTT	960
GGTGTTCCGG	CGATTTTGTT	GTGGAACAAG	GGGAAAGATC	GTAGACGGTC	TAAGTATAAG	1020
CTTGTTTATA	CCGTTAGGAC	TCATAAAGGA	GCTGTTGAGA	AGGCTTTCAA	CTGTGTTTAC	1080
CAAGAGCAAG	ATGATAATGG	GAAGACCGGG	GTTTCGTTGT	CGAAAGATCT	TATGGCTATA	1140
GCTGGGGAAG	CTCTTAAGGC	GAATATCACT	ACTTTAGGTC	CTTTGGTTCT	TCCTATAAGT	1200
GAGCAGATTC	TGTTTTTTCAT	GACTTTGGTT	ACGAAGAAAC	TGTTTAACTC	GAAGCTGAAG	1260
CCGTATATTC	CGGATTTCAA	GCTTGCGTTT	GATCATTTCT	GTATCCATGC	TGGTGGTAGA	1320
GCTGTGATTG	ATGAGCTTGA	GAAGAATCTG	CAGCTTTCGC	AGACTCATGT	CGAGGCATCC	1380
AGAATGACAC	TGCACAGATT	TGGAAACACT	TCTTCGAGCT	CGATTGGTA	TGAACCTGGC	1440
TACATAGAGG	CTAAAGGTAG	GATGAAGAAA	GGAAACCGGG	TTTGGCAGAT	TGCTTTTGGA	1500
AGTGGGTTTA	AGTGTAACAG	TGCAGTTTGG	GTGGCTCTAA	ACAATGTCAA	GCCTTCGGTT	1560
AGTAGTCCGT	GGGAACACTG	CATCGACCGA	TATCCGGTTA	AGCTCGACTT	C	1611

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser	Ser	Tyr	Val	Arg	Ala	Phe	Ile	Cys	Thr	Asn	Ser	His	Lys	Val	Phe
1				5				10					15		
Asn	Phe	Ile	Pro	Phe	Phe	Ser	Glu	Ala	Met	Glu	Ala	Ala	Asn	Glu	Pro
		20					25					30			
Val	Asn	Gly	Gly	Ser	Val	Gln	Ile	Arg	Thr	Glu	Asn	Asn	Glu	Arg	Arg
	35					40					45				
Lys	Leu	Pro	Asn	Phe	Leu	Gln	Ser	Val	Asn	Met	Lys	Tyr	Val	Lys	Leu
	50				55				60						
Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Leu	Phe	Lys	Leu	Cys	Leu	Val	Pro
65				70				75					80		
Leu	Met	Ala	Val	Leu	Val	Thr	Glu	Ile	Ser	Arg	Leu	Thr	Thr	Asp	Asp
			85					90					95		
Leu	Tyr	Gln	Ile	Trp	Leu	His	Leu	Gln	Tyr	Asn	Leu	Val	Ala	Phe	Ile
	100						105					110			
Phe	Leu	Ser	Ala	Leu	Ala	Ile	Phe	Gly	Ser	Thr	Val	Tyr	Ile	Met	Ser
	115					120					125				
Arg	Pro	Arg	Ser	Val	Tyr	Leu	Val	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro
	130					135				140					
Glu	Ser	Leu	Gln	Val	Lys	Tyr	Gln	Lys	Phe	Met	Asp	His	Ser	Lys	Leu
145				150				155						160	
Ile	Glu	Asp	Phe	Asn	Glu	Ser	Ser	Leu	Glu	Phe	Gln	Arg	Lys	Ile	Leu
			165					170					175		
Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	Glu	Ala	Leu	His
			180					185					190		

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Cys Ile Pro Pro Arg Pro Thr Met Met Ala Ala Arg Glu Glu Ser Glu
 195 200 205
 Gln Val Met Phe Gly Ala Leu Asp Lys Leu Phe Glu Asn Thr Lys Ile
 210 215 220
 Asn Pro Arg Asp Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn
 225 230 235 240
 Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg
 245 250 255
 Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala Gly
 260 265 270
 Val Ile Ser Ile Asp Leu Ala Lys Asp Met Leu Gln Val His Arg Asn
 275 280 285
 Thr Tyr Ala Val Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp Tyr
 290 295 300
 Phe Gly Asn Lys Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg Val
 305 310 315 320
 Gly Gly Ser Ala Ile Leu Leu Ser Asn Lys Gly Lys Asp Arg Arg Arg
 325 330 335
 Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ala Val
 340 345 350
 Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu Gln Asp Asn Gly Lys
 355 360 365
 Thr Gly Val Ser Leu Ser Lys Asp Leu Met Ala Ile Ala Gly Glu Ala
 370 375 380
 Leu Lys Ala Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile Ser
 385 390 395 400
 Glu Gln Ile Leu Phe Met Thr Leu Val Thr Lys Lys Leu Phe Asn
 405 410 415
 Ser Lys Leu Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Asp His
 420 425 430
 Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu Leu Glu Lys
 435 440 445
 Asn Leu Gln Leu Ser Gln Thr His Val Glu Ala Ser Arg Met Thr Leu
 450 455 460
 His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala
 465 470 475 480
 Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Arg Val Trp Gln
 485 490 495
 Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Val Ala
 500 505 510
 Leu Asn Asn Val Lys Pro Ser Val Ser Ser Pro Trp Glu His Cys Ile
 515 520 525
 Asp Arg Tyr Pro Val Lys Leu Asp Phe
 530 535

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCGACGA	TGCCTCAGGC	ACCGATGCCA	GAGTTCTCTA	GCTCGGTGAA	GCTCAAGTAC	60
GTGAAACTTG	GTTACCAATA	TTTGGTTAAC	CATTTCTTGA	GTTTTCTTTT	GATCCCGATC	120
ATGGCTATTG	TCGCCGTTGA	GCTTCTTCGG	ATGGGTCCTG	AAGAGATCCT	TAATGTTTGG	180
AATTCACTCC	AGTTTGACCT	AGTTCAGGTT	CTATGTTCTT	CCTTCTTTGT	CATCTTCATC	240
TCCACTGTTT	ACTTCATGTC	CAAGCCACGC	ACCATCTACC	TCGTTGACTA	TTCTTGTTAC	300
AAGCCACCTG	TCACGTGTCG	TGTCCCTTTC	GCAACTTTCA	TGGAACACTC	TCGTTTGATC	360
CTCAAGGACA	AGCCTAAGAG	CGTCGAGTTC	CAAATGAGAA	TCCTTGAACG	TTCTGGCCTC	420
GGTGAGGAGA	CTTGTCTCCC	TCCGGCTATT	CATTATATTC	CTCCACACAC	AACCATGGAC	480
GCGGCTAGAA	GCGAGGCTCA	GATGGTTATC	TTCGAGGCCA	TGGACGATCT	TTTCAAGAAA	540
ACCGGTCTTA	AACCTAAAGA	CGTCGACATC	CTTATCGTCA	ACTGCTCTCT	TTTCTCTCCC	600

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ACACCATCGC	TCTCAGCTAT	GGTCATCAAC	AAATATAAGC	TTAGGAGTAA	TATCAAGAGC	660
TTCAATCTTT	CGGGGATGGG	CTGCAGCGCG	GGCCTGATCT	CAGTTGATCT	AGCCCAGCAG	720
TTGCTCCAAG	TTCATCCCAA	TTCAAATGCA	ATCATCGTCA	GCACGGAGAT	CATAACGCCT	780
AATTACTATC	AAGGCAACGA	GAGAGCCATG	TTGTTACCCA	ATTGTCTCTT	CCGCATGGGT	840
GCGGCAGCCA	TACACATGTC	AAACCGCCGG	TCTGACCGGT	GGCGAGCCAA	ATACAAGCTT	900
TCCCACCTCG	TCCGGACACA	CCGTGGCGCT	GACGACAAGT	CTTTCTACTG	TGTCTACGAA	960
CAGGAAGACA	AAGAAGGACA	CGTTGGCATC	AACTTGTCCA	AAGATCTCAT	GGCCATCGCC	1020
GGTGAAGCCC	TCAAGGCCAA	CATCACCACA	ATAGGTCCTT	TGGTCCTACC	GGCGTCAGAA	1080
CAACTTCTCT	TCCTCACGTC	CCTAATCGGA	CGTAAAATCT	TCAACCCGAA	ATGGAAACCA	1140
TACATACCGG	ATTTCAAGCT	GGCCTTCGAA	CACTTTTGCA	TTCACGCAGG	AGGCAGAGCG	1200
GTGATCGACG	AGCTCCAAA	GAATCTACAA	CTATCAGGAG	AACACGTTGA	GGCCTCAAGA	1260
ATGACACTAC	ATCGTTTTGG	TAACACGTCA	TCTTCATCGT	TATGGTACGA	GCTTAGCTAC	1320
ATCGAGTCTA	AAGGGAGAAT	GAGGAGAGGC	GATCGCGTTT	GGCAAATCGC	GTTTGGGAGT	1380
GGTTTCAAGT	GTAACCTCTG	CGTGTGGAAG	TGTAACCGTA	CGATTAAGAC	ACCTAAGGAC	1440
GGACCATGGT	CCGATTGTAT	CGACCGTTAC	CCTGTCTTTA	TTCCCGAAGT	TGTCAAATCT	1500
TA						1502

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser	Pro	Thr	Met	Pro	Gln	Ala	Pro	Met	Pro	Glu	Phe	Ser	Ser	Ser	Val
1				5					10					15	
Lys	Leu	Lys	Tyr	Val	Lys	Leu	Gly	Tyr	Gln	Tyr	Leu	Val	Asn	His	Phe
			20					25					30		
Leu	Ser	Phe	Leu	Leu	Ile	Pro	Ile	Met	Ala	Ile	Val	Ala	Val	Glu	Leu
		35					40					45			
Leu	Arg	Met	Gly	Pro	Glu	Glu	Ile	Leu	Asn	Val	Trp	Asn	Ser	Leu	Gln
	50					55				60					
Phe	Asp	Leu	Val	Gln	Val	Leu	Cys	Ser	Ser	Phe	Phe	Val	Ile	Phe	Ile
65					70					75					80
Ser	Thr	Val	Tyr	Phe	Met	Ser	Lys	Pro	Arg	Thr	Ile	Tyr	Leu	Val	Asp
				85				90					95		
Tyr	Ser	Cys	Tyr	Lys	Pro	Pro	Val	Thr	Cys	Arg	Val	Pro	Phe	Ala	Thr
			100					105					110		
Phe	Met	Glu	His	Ser	Arg	Leu	Ile	Leu	Lys	Asp	Lys	Pro	Lys	Ser	Val
		115					120					125			
Glu	Phe	Gln	Met	Arg	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr
		130					135				140				
Cys	Leu	Pro	Pro	Ala	Ile	His	Tyr	Ile	Pro	Pro	Thr	Pro	Thr	Met	Asp
145					150					155					160
Ala	Ala	Arg	Ser	Glu	Ala	Gln	Met	Val	Ile	Phe	Glu	Ala	Met	Asp	Asp
				165						170				175	
Leu	Phe	Lys	Lys	Thr	Gly	Leu	Lys	Pro	Lys	Asp	Val	Asp	Ile	Leu	Ile
			180					185					190		
Val	Asn	Cys	Ser	Leu	Phe	Ser	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val
		195					200					205			
Ile	Asn	Lys	Tyr	Lys	Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Ser
		210				215					220				
Gly	Met	Gly	Cys	Ser	Ala	Gly	Leu	Ile	Ser	Val	Asp	Leu	Ala	Arg	Asp
225					230					235					240
Leu	Leu	Gln	Val	His	Pro	Asn	Ser	Asn	Ala	Ile	Ile	Val	Ser	Thr	Glu
				245						250				255	
Ile	Ile	Thr	Pro	Asn	Tyr	Tyr	Gln	Gly	Asn	Glu	Arg	Ala	Met	Leu	Leu
			260					265					270		
Pro	Asn	Cys	Leu	Phe	Arg	Met	Gly	Ala	Ala	Ala	Ile	His	Met	Ser	Asn
		275					280					285			
Arg	Arg	Ser	Asp	Arg	Trp	Arg	Ala	Lys	Tyr	Lys	Leu	Ser	His	Leu	Val
			290				295				300				

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Arg Thr His Arg Gly Ala Asp Asp Lys Ser Phe Tyr Cys Val Tyr Glu
 305 310 315 320
 Gln Glu Asp Lys Gly His Val Gly Ile Asn Leu Ser Lys Asp Leu
 325 330 335
 Met Ala Ile Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Ile Gly
 340 345 350
 Pro Leu Val Leu Pro Ala Ser Glu Gln Leu Leu Phe Leu Thr Ser Leu
 355 360 365
 Ile Gly Arg Lys Ile Phe Asn Pro Lys Trp Lys Pro Tyr Ile Pro Asp
 370 375 380
 Phe Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala
 385 390 395 400
 Val Ile Asp Glu Leu Gln Lys Asn Leu Gln Leu Ser Gly Glu His Val
 405 410 415
 Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser
 420 425 430
 Ser Leu Trp Tyr Glu Leu Ser Tyr Ile Glu Ser Lys Gly Arg Met Arg
 435 440 445
 Arg Gly Asp Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys
 450 455 460
 Asn Ser Ala Val Trp Lys Cys Asn Arg Thr Ile Lys Thr Pro Lys Asp
 465 470 475 480
 Gly Pro Trp Ser Asp Cys Ile Asp Arg Tyr Pro Val Phe Ile Pro Glu
 485 490 495
 Val Val Lys Leu
 500

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGGACGGTG	CCGGAGAATC	ACGACTCGGT	GGTGATGGTG	GTGGTGATGG	TTCTGTTGGA	60
GTTTCAGATCC	GACAAACACG	GATGCTACCG	GATTTTCTCC	AGAGCGTGAA	TCTCAAGTAT	120
GTGAAATTAG	GTTACCATTA	CTTAATCTCA	AATCTCTTGA	CTCTCTGTTT	ATTCCCTCTC	180
GCCGTTGTTA	TCTCCGTCGA	AGCCTCTCAG	ATGAACCCAG	ATGATCTCAA	ACAGCTCTGG	240
ATCCATCTAC	AATACAATCT	GGTTAGTATC	ATCATCTGTT	CAGCGATTCT	AGTCTTCGGG	300
TTAACGGTTT	ATGTTATGAC	CCGACCTAGA	CCCGTTTACT	TGTTTGATTT	CTCTTGTTAT	360
CTCCCACCTG	ATCATCTCAA	AGCTCCTTAC	GCTCGGTTCA	TGGAACATTG	TAGACTCACC	420
GGAGATTTCG	ATGACTCTGC	TCTCGAGTTT	CAACGCAAGA	TCCTTGAGCG	TTCTGGTTTA	480
GGGGAAGACA	CTTATGTCCC	TGAAGCTATG	CATTATGTTT	CACCGAGAAT	TTCAATGGCT	540
GCTGCTAGAG	AAGAAGCTGA	ACAAGTCATG	TTTGGTGCTT	TAGATAACCT	TTTCGCTAAC	600
ACTAATGTGA	AACCAAAGGA	TATTGGAATC	CTTGTTGTGA	ATTGTAGTCT	CTTTAATCCA	660
ACTCCTTCGT	TATCTGCAAT	GATTGTGAAC	AAGTATAAGC	TTAGAGGTAA	CATTAGAAGC	720
TACAATCTAG	GCGGTATGGG	TTGCAGCGCG	GGAGTTATCG	CTGTGGATCT	TGCTAAAGAC	780
ATGTTGTTGG	TACATAGGAA	CACTTATGCG	GTTGTTGTTT	CTACTGAGAA	CATTACTCAG	840
AATTGGTATT	TTGGTAACAA	GAAATCGATG	TTGATACCGA	ACTGCTTGTT	TCGAGTTGGT	900
GGCTCTGCGG	TTTTGCTATC	GAACAAGTCG	AGGGACAAGA	GACGGTCTAA	GTACAGGCTT	960
GTACATGTAG	TCAGGACTCA	CCGTGGAGCA	GATGATAAAG	CTTTCGGTTG	TGTTTATCAA	1020
GAGCAGGATG	ATACAGGGAG	AACCGGGGTT	TCGTTGTCTGA	AAGATCTAAT	GGCGATTGCA	1080
GGGGAACCTC	TCAAAACCAA	TATCACTACA	TTGGGTCCTC	TTGTTCTACC	GATAAGTGAG	1140
CAGATTCTCT	TCTTTATGAC	TCTAGTTGTG	AAGAAGCTCT	TTAACGGTAA	AGTGAAACCG	1200
TATATCCCGG	ATTTCAAACCT	TGCTTTTCGAG	CATTTCTGTA	TCCATGCTGG	TGGAAGAGCT	1260
GTGATCGATG	AGTTAGAGAA	GAATCTGCAG	CTTTCACCAG	TTCATGTCTGA	GGCTTCGAGG	1320
ATGACTCTTC	ATCGATTGTT	TAACACATCT	TCGAGCTCCA	TTTGGTATGA	ATTGGCTTAC	1380
ATTGAAGCGA	AGGGAAGGAT	GCGAAGAGGT	AATCGTGTTT	GGCAAATCGC	GTTTCGGAAGT	1440
GGATTTAAT	GTAATAGCGC	GATTTGGGAA	GCATTAAGGC	ATGTGAAACC	TTCGAACAAC	1500
AGTCCTTGGG	AAGATTGTAT	TGACAAGTAT	CCGGTAACTT	TAAGTTAT		1548

(2) INFORMATION FOR SEQ ID NO:14:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Met Asp Gly Ala Gly Glu Ser Arg Leu Gly Gly Asp Gly Gly Gly Asp
 1      5      10      15
Gly Ser Val Gly Val Gln Ile Arg Gln Thr Arg Met Leu Pro Asp Phe
 20      25      30
Leu Gln Ser Val Asn Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu
 35      40      45
Ile Ser Asn Leu Leu Thr Leu Cys Leu Phe Pro Leu Ala Val Val Ile
 50      55      60
Ser Val Glu Ala Ser Gln Met Asn Pro Asp Asp Leu Lys Gln Leu Trp
 65      70      75      80
Ile His Leu Gln Tyr Asn Leu Val Ser Ile Ile Cys Ser Ala Ile
 85      90      95
Leu Val Phe Gly Leu Thr Val Tyr Val Met Thr Arg Pro Arg Pro Val
100      105      110
Tyr Leu Val Asp Phe Ser Cys Tyr Leu Pro Pro Asp His Leu Lys Ala
115      120      125
Pro Tyr Ala Arg Phe Met Glu His Ser Arg Leu Thr Gly Asp Phe Asp
130      135      140
Asp Ser Ala Leu Glu Phe Gln Arg Lys Ile Leu Glu Arg Ser Gly Leu
145      150      155      160
Gly Glu Asp Thr Tyr Val Pro Glu Ala Met His Tyr Val Pro Pro Arg
165      170      175
Ile Ser Met Ala Ala Ala Arg Glu Glu Ala Glu Gln Val Met Phe Gly
180      185      190
Ala Leu Asp Asn Leu Phe Ala Asn Thr Asn Val Lys Pro Lys Asp Ile
195      200      205
Gly Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu
210      215      220
Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly Asn Ile Arg Ser
225      230      235      240
Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ala Val Asp
245      250      255
Leu Ala Lys Asp Met Leu Leu Val His Arg Asn Thr Tyr Ala Val Val
260      265      270
Val Ser Thr Glu Asn Ile Thr Gln Asn Trp Tyr Phe Gly Asn Lys Lys
275      280      285
Ser Met Leu Ile Pro Asn Cys Leu Phe Arg Val Gly Gly Ser Ala Val
290      295      300
Leu Leu Ser Asn Lys Ser Arg Asp Lys Arg Arg Ser Lys Tyr Arg Leu
305      310      315      320
Val His Val Val Arg Thr His Arg Gly Ala Asp Asp Lys Ala Phe Arg
325      330      335
Cys Val Tyr Gln Glu Gln Asp Asp Thr Gly Arg Thr Gly Val Ser Leu
340      345      350
Ser Lys Asp Leu Met Ala Ile Ala Gly Glu Thr Leu Lys Thr Asn Ile
355      360      365
Thr Thr Leu Gly Pro Leu Val Leu Pro Ile Ser Glu Gln Ile Leu Phe
370      375      380
Phe Met Thr Leu Val Val Lys Lys Leu Phe Asn Gly Lys Val Lys Pro
385      390      395      400
Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys Ile His Ala
405      410      415
Gly Gly Arg Ala Val Ile Asp Glu Leu Lys Asn Leu Gln Leu Ser
420      425      430
Pro Val His Val Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn
435      440      445

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[illegible]

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WHAT IS CLAIMED IS:

1. An isolated polynucleotide encoding a polypeptide having an amino acid sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an amino acid sequence substantially identical to SEQ ID NO:14.
2. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:2.
3. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:4.
4. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:6.
5. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:8.
6. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:10.
7. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:12.
8. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:14.

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9. An isolated polynucleotide, wherein said polynucleotide is selected from the group consisting of:

- a) SEQ ID NO:1;
- b) SEQ ID NO:3;
- c) SEQ ID NO:5;
- d) SEQ ID NO:7;
- e) SEQ ID NO:9;
- f) SEQ ID NO:11;
- g) SEQ ID NO:13;
- h) an RNA analog of SEQ ID NO:1;
- i) an RNA analog of SEQ ID NO:3;
- j) an RNA analog of SEQ ID NO:5;
- k) an RNA analog of SEQ ID NO:7;
- l) an RNA analog of SEQ ID NO:9;
- m) an RNA analog of SEQ ID NO:11;
- n) an RNA analog of SEQ ID NO:13;
- o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
- p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

10. An isolated polypeptide having an amino acid sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an

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amino acid sequence substantially identical to SEQ ID NO:14.

11. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:2.

12. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:4.

13. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:6.

14. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:8.

15. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:10.

16. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:12.

17. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:14.

18. A transgenic plant containing a nucleic acid construct comprising a polynucleotide selected from the group consisting of:

- a) SEQ ID NO:1;
- b) SEQ ID NO:3;
- c) SEQ ID NO:5;
- d) SEQ ID NO:7;
- e) SEQ ID NO:9;
- f) SEQ ID NO:11;
- g) SEQ ID NO:13;
- h) an RNA analog of SEQ ID NO:1;

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- i) an RNA analog of SEQ ID NO:3;
- j) an RNA analog of SEQ ID NO:5;
- k) an RNA analog of SEQ ID NO:7;
- l) an RNA analog of SEQ ID NO:9;
- m) an RNA analog of SEQ ID NO:11;
- n) an RNA analog of SEQ ID NO:13;
- o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
- p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

19. The plant of claim 18, wherein said construct further comprises a regulatory element operably linked to said polynucleotide.

20. The plant of claim 19, wherein said regulatory element is a tissue-specific promoter.

21. The plant of claim 20, wherein said regulatory element is an epidermal cell-specific promoter.

22. The plant of claim 20, wherein said regulatory element is a seed-specific promoter that is operably linked in sense orientation to said polynucleotide.

23. The plant of claim 22, wherein said plant has altered levels of very long chain fatty acids in seeds compared to the levels in a plant lacking said nucleic acid construct.

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linked. Examples of regulatory sequences are known in the art and include, without limitation, minimal promoters and promoters of genes preferentially or exclusively expressed in seeds or in epidermal cells of stems and leaves. Native regulatory sequences of the polynucleotides disclosed herein can be readily isolated by those skilled in the art and used in constructs of the invention. Other examples of suitable regulatory sequences include enhancers or enhancer-like elements, introns, 3' non-coding regions such as poly A sequences and other regulatory sequences discussed herein. Molecular biology techniques for preparing such chimeric genes are known in the art.

In other embodiments, a transgenic plant contains a nucleic acid construct comprising a partial or a full-length KAS coding sequence operably linked to at least one suitable regulatory sequence in antisense orientation. The chimeric gene can be introduced into a plant and transgenic progeny displaying expression of the antisense construct are identified.

One may use a polynucleotide disclosed herein for cosuppression as well as for antisense inhibition. Cosuppression of genes in plants may be achieved by expressing, in the sense orientation, the entire or partial coding sequence of a gene. See, e.g., WO 04/11516, incorporated herein by reference.

Transgenic techniques for use in the invention include, without limitation, *Agrobacterium*-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation. Illustrative examples of transformation techniques are described in U.S. Patent 5,204,253, (particle gun) and U.S. Patent 5,188,958 (*Agrobacterium*), incorporated herein by reference. Transformation methods utilizing the Ti and Ri plasmids of *Agrobacterium* spp. typically

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use binary-type vectors. Walkerpeach, C. et al., in Plant Molecular Biology Manual, S. Gelvin and R. Schilperoort, eds., Kluwer Dordrecht, C1:1-19 (1994). If cell or tissue cultures are used as the recipient tissue
5 for transformation, plants can be regenerated from transformed cultures by techniques known to those skilled in the art.

Techniques are known for the introduction of DNA into monocots as well as dicots, as are the techniques
10 for culturing such plant tissues and regenerating those tissues. Monocots which have been successfully transformed and regenerated include wheat, corn, rye, rice, and asparagus. See, e.g., U.S. Patent Nos. 5,484,956 and 5,550,318, incorporated herein by
15 reference.

For efficient production of transgenic plants from plant cells, it is desirable that the plant tissue used for transformation possess a high capacity for regeneration. Transgenic plants of woody species such as
20 poplar and aspen have also been obtained. Technology is also available for the manipulation, transformation, and regeneration of gymnosperm plants. For example, U.S. Patent No. 5,122,466 describes the biolistic transformation of conifers, with preferred target tissue
25 being meristematic and cotyledon and hypocotyl tissues. U.S. Patent No. 5,041,382 describes enrichment of conifer embryonal cells.

Seeds produced by a transgenic plant(s) can be grown and then selfed (or outcrossed and selfed) to
30 obtain seeds homozygous for the construct. Seeds can be analyzed in order to identify those homozygotes having the desired expression of the construct. Transgenic plants may be entered into a breeding program, e.g., to introgress the novel construct into other lines, to
35 transfer the construct to other species, or for further

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selection of other desirable traits. Alternatively, transgenic plants may be propagated vegetatively for those species amenable to such techniques. A nucleic acid construct of the invention can alter the levels of very long chain fatty acids in plant tissues expressing the polynucleotide, compared to VLCFA levels in corresponding tissues from an otherwise identical plant not expressing the polynucleotide. A comparison can be made, for example, between a non-transgenic plant of a plant line and a transgenic plant of the same plant line. Levels of VLCFAs having 20-32 carbons and/or levels of VLCFAs having 32-60 carbons can be altered in plants disclosed herein. Plants having an altered VLCFA composition may be identified by techniques known to the skilled artisan, e.g., thin layer chromatography or gas-liquid chromatography (GLC) analysis of the appropriate plant tissue.

A suitable group of plants with which to practice the invention are the *Brassica* species, including *B. napus*, *B. rapa*, *B. juncea*, and *B. hirta*. Other suitable plants include, without limitation, soybean (*Glycine max*), sunflower (*Helianthus annuus*) and corn (*Zea mays*).

A method according to the invention comprises introducing a nucleic acid construct into a plant cell and producing a plant (as well as progeny of such a plant) from the transformed cell. Progeny includes descendants of a particular plant or plant line, e.g., seeds developed on an instant plant are descendants. Progeny of an instant plant include seeds formed on F_1 , F_2 , F_3 , and subsequent generation plants, or seeds formed on BC_1 , BC_2 , BC_3 , and subsequent generation plants.

Methods and compositions according to the invention are useful in that the resulting plants and plant lines have desirable alterations in very long chain fatty acid composition. Suitable tissues in which to

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express polynucleotides and/or polypeptides of the invention include, without limitation, seeds, stems and leaves. Leaf tissues of interest include cells and tissues of the epidermis, e.g., cells that are involved
5 in forming trichomes. Of particular interest are epidermal cells involved in forming the cuticular layer. The cuticular layer comprises various very long chain fatty acids and VLCFA derivatives such as alkanes, esters, alcohols and aldehydes. Altering the composition
10 and amount of VLCFAs in epidermal cells and tissues may enhance defense mechanisms and drought tolerance of plants disclosed herein.

Polynucleotides of the invention can be used as markers in plant genetic mapping and plant breeding
15 programs. Such markers may include RFLP, RAPD, or PCR markers, for example. Marker-assisted breeding techniques may be used to identify and follow a desired fatty acid composition during the breeding process. Marker-assisted breeding techniques may be used in
20 addition to, or as an alternative to, other sorts of identification techniques. An example of marker-assisted breeding is the use of PCR primers that specifically amplify a sequence from a desired KAS that has been introduced into a plant line and is being crossed into
25 other plant lines.

Plants and plant lines disclosed herein preferably have superior agronomic properties. Superior agronomic characteristics include, for example, increased seed germination percentage, increased seedling vigor,
30 increased resistance to seedling fungal diseases (damping off, root rot and the like), increased yield, and improved standability.

While the invention is susceptible to various modifications and alternative forms, certain specific
35 embodiments thereof are described in the general methods

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and examples set forth below. It should be understood, however, that these examples are not intended to limit the invention to the particular forms disclosed but, instead the invention is to cover all modifications, 5 equivalents and alternatives falling within the scope of the invention.

EXAMPLES

Example 1

Cloning and Expression of FAE1 in Yeast Cells

10 The open reading frame of the *Arabidopsis* FAE1 gene was amplified directly by PCR, using *Arabidopsis thaliana* cv. Columbia genomic DNA as a template, pfu DNA polymerase and the following primers:

5'CTCGAGGAGCAATGACGTCCGTAA-3' and 5'-

15 CTCGAGTTAGGACCGACCGTTTGTG-3'. The PCR product was blunt-end cloned into the *Eco* RV site of pBluescript (Stratagene, La Jolla, CA),

 The FAE1 gene was excised from the Bluescript vector with *Bam*HI, and then subcloned into the pYEura3 20 (Clontech, Palo Alto, CA). pYEura3 is a yeast centromere-containing, episomal plasmid that is propagated stably through cell division. The FAE1 gene was inserted downstream of a GAL1 promoter in pYEura3. The GAL1 promoter is induced when galactose is present in 25 the medium and repressed when glucose is present in the growth medium.

 Insertion of the FAE1 gene in the sense orientation was confirmed by PCR, and pYEura3/FAE1 was used to transform *Saccharomyces cerevisiae* strain AB1380 30 using a lithium acetate procedure as described in Gietz, R. and Woods, R., in *Molecular Genetics of Yeast: Practical Approaches*, Oxford Press, pp. 121-134 (1994). Plasmid DNA was isolated from putative transformants, and

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the presence of the *FAE1*/pYEUra3 construct was confirmed by Southern analysis.

Yeast transformed with pYEUra3 having *FAE1* operably linked to the *GAL1* promoter were grown in the presence of galactose or glucose and were analyzed for the expression of *FAE1*. As a control, yeast transformed with pYEUra3 containing no insert were also assayed. Analysis of such control preparations yielded fatty acid compositions and fatty acid elongation rates similar to those of yeast transformed with pYEUra3/*FAE1* and grown with glucose as the carbon source.

The fatty acid composition of yeast cells grown in the presence of galactose was compared to that of cells grown in the presence of glucose, to determine if VLCFA were found in the galactose-induced cells.

Transformed yeast cells were grown overnight in YPD media at 30°C with vigorous shaking. One hundred μ l of the overnight culture were used to inoculate 40 ml of complete minimal uracil dropout media (CM-Ura) supplemented with either glucose or galactose (2% w/v). Cultures were grown at 30°C to an OD₆₀₀ of approximately 1.3 to 1.5. Cells were harvested by centrifugation at 5000 Xg for 10 min. Total lipids were extracted from the cells with 2 volumes of 4N KOH in 100% methanol for 60 min. at 80°C. Fatty acids were saponified and methyl esters were prepared by drying the samples and resuspending in 0.5 ml of boron trichloride in methanol (10% v/v). Samples were incubated at 50°C for 15 min in a sealed tube. About 2 ml of water was then added and the fatty methyl esters were extracted thrice with 1 ml of hexane. Extracts were dried under nitrogen and redissolved in hexane. See Hlousek-Radojcic, A. et al., Plant J. 8:803-809. Methyl esters were analyzed on an HP 5890 series II gas chromatograph equipped with a 5771MSD and 7673 auto injector (Hewlett-Packard, Cincinnati, OH).

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Methyl esters were separated on a DB-23 (J&W Scientific) capillary column (30 m X 0.25 mm X 0.25 μ m). The column was operated with helium carrier gas and splitless injection (injection temperature 280°C, detector temperature 280°C). After an initial 3 min. at 100°C, the oven temperature was raised to 250° at 20°C min⁻¹ and maintained at that temperature for an additional 3 min. The identity of the peaks was verified by cochromatography with authentic standards and by mass spectrometer analysis.

The results clearly revealed the appearance of both 20:1 and 22:1 acyl-CoA products in galactose-induced yeast containing the *FAE1* coding sequence. Uninduced yeast cells failed to accumulated significant amounts of fatty acids longer than C18. These results indicate that expression of *FAE1* in yeast resulted in functional KAS activity and functional elongase activity.

Example 2

***FAE1* Activity in Yeast Microsomes**

The functional expression of the *FAE1* KAS was analyzed by isolating microsomes from transformed yeast cells and assaying these microsomes *in vitro* for elongase activity.

Transformed yeast cells were grown in the presence of either glucose or galactose (2% w/v) as described in Example 1. Cells were harvested by centrifugation at 5000 Xg for 10 min and washed with 10 ml ice cold isolation buffer (IB), which contains 80 mM Hepes-KOH, pH 7.2, 5 mM EGTA, 5 mM EDTA, 10 mM KCl, 320 mM sucrose and 2 mM DTT). Cells were then resuspended in enough IB to fill a 1.7 ml tube containing 700 μ l of 0.5 μ m glass beads and yeast microsomes were isolated from the cells essentially as described in Tillman, T. and Bell, R., J. Biol. Chem. 261:9144-9149 (1986). The microsomal

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membrane pellet was recovered by centrifugation at 252,000 xg for 60 min. The pellet was rinsed by resuspending in 40 ml fresh IB and again recovered by centrifugation at 252000 Xg for 60 min. Microsomal
5 pellets were resuspended in a minimal volume of IB, and the protein concentration adjusted to $2.5 \mu\text{g } \mu\text{l}^{-1}$ by addition of IB containing 15% glycerol. Microsomes were frozen on dry ice and stored at -80°C . The protein concentration in microsomes was determined by the
10 Bradford method (Bradford, 1976).

Fatty acid elongase activity was measured essentially as described in Hlousek-Radojcic, A. et al., Plant J. 8:803-809 (1995). Briefly, the standard elongation reaction mix contained 80 mM Hepes-KOH, pH
15 7.2, 20 mM MgCl_2 , 500 μM NADPH, 1 mM ATP, 100 μM malonyl-CoA, 10 μM CoA-SH and 15 μM radioactive acyl-CoA substrate. The radiolabeled substrate was either [$1\text{-}^{14}\text{C}$]18:1-CoA (50 uCi μmol^{-1}), [$1\text{-}^{14}\text{C}$]18:0-CoA (55 uCi μmol^{-1}), or [$1\text{-}^{14}\text{C}$]16:0-CoA (54 uCi μmol^{-1}). The reaction was
20 initiated by the addition of yeast microsomes (5 μg protein) and the mixture incubated at 30°C for the indicated period of time. The final reaction volume was 25 μl .

Methyl esters of the acyl-CoA elongation products
25 were prepared as described in Example 1. Methyl esters were separated on reversed phase silica gel KC18 TLC plates (Whatman, 250 μM thick), quantified by phosphorimaging, and analyzed on by ImageQuant software (Molecular Dynamics, Inc., Sunnyvale, CA). The detection
30 limit for each product is about 0.001 nanomoles per min. per mg microsomal protein, depending on the phosphorimage exposure time.

Results of representative *in vitro* elongation assays are shown in Figs. 1 and 2. The results indicate
35 that microsomes from galactose-induced cells expressing

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FAE1 catalyzed multiple cycles of elongation starting with either C16:0 acyl CoA, C18:0 acyl CoA, or C18:1 acyl-CoA as the substrate (Fig. 1). The 16:0 and 18:0 acyl-CoA substrates were elongated to C26:0 acyl-CoA. In contrast, the 18:1-CoA substrate was elongated primarily to C20:1, with only low levels of C22:1 acyl-CoA being produced. Occasionally, trace levels of C24:1 CoA were also observed. Although the chain length of the products from the 18:1 acyl-CoA substrate were less than the chain length from the saturated acyl-CoA substrates, the rate of elongation of oleoyl-CoA was about 2- and 3-fold higher than the rates of elongation of 16:0-CoA and 18:0-CoA, respectively.

The elongation activity observed in microsomes from uninduced cells indicated that there was a low level of endogenous elongase activity when 18:1-CoA or 18:0-CoA were used as substrates. There was substantial 16:0-CoA elongase activity (10.1 nmol mg protein⁻¹ at 30 min) in microsomes from uninduced cells (Fig. 2). However, the major product of 16:0 elongation using uninduced microsomes was C18:0 acyl CoA, with only small amounts of products beyond this length. The elongation of the 16:0 acyl-CoA substrate presumably is due to an endogenous yeast elongase.

Elongation of 18:1 CoA by microsomes from induced cells occurred at a rate about 18-fold higher than in microsomes isolated from the uninduced cells (Fig. 2). With microsomes from induced yeast, synthesis of 20:0 CoA from the 16:0 CoA substrate, occurred at a rate similar to that seen when the substrate was 18:0 CoA (4.2 vs. 5.1 nmol mg protein⁻¹). The total rate of elongation of [¹⁴C] 16:0-CoA by microsomes from induced cells (15.8 nmol mg protein⁻¹ at 30 min.) was more than 50% higher than elongation of [¹⁴C] 16:0-CoA by microsomes from uninduced cells, suggesting that the *FAE1* KAS utilized 16:0-CoA as

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a substrate in addition to C18-C24 acyl-CoAs. The *FAE1* elongase KAS activity, i.e., the difference in the 16:0 elongation rates between microsomes from induced and uninduced cells, was 5.7 nmol mg protein⁻¹. The
5 elongation rate with the 16:0 substrate thus was similar to the elongase activity of the *FAE1* elongase KAS with the 18:0 substrate.

These results indicate that *FAE1* KAS expressed in yeast could synthesize 3-ketoacyl-CoA *in vitro* and, in
10 combination with yeast reductases and dehydrases, could form a functional VLCFA elongase complex. In addition, these results suggest that *FAE1* is membrane-bound in yeast cells.

Example 3

15 **Cloning and Sequencing of Arabidopsis Elongase Genes**

The sequence of a jojoba seed cDNA (see WO 93/10241 and WO 95/15387, incorporated herein by reference) was used to search the Arabidopsis expressed sequence tag (EST) database of the Arabidopsis Genome
20 Stock Center (The Ohio State University, Columbus, Ohio). The BLAST computer program (National Institutes of Health, Bethesda, MD, USA) was used to perform the search. The search identified two ESTs (ATTS1282 and ATTS3218) that had a high degree of sequence identity
25 with the jojoba sequence. The ATTS1282 and ATTS3218 ESTs appeared to be partial cDNA clones rather than full-length clones based on the length of the jojoba sequence.

A genomic DNA library from *Arabidopsis thaliana* cv. Columbia, was prepared in the lambda GEM11 vector
30 (Promega, Madison, Wisconsin) and was obtained from Ron Davis, Stanford University, Stanford, CA. The library was hybridized with ATTS1282 and ATTS3218 as probes and 2 clones were identified for each EST. Phage DNA was isolated from each of the hybridizing clones, the genomic

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insert was excised with the restriction enzyme Sac I and subcloned into the plasmid pBluescript (Stratagene, La Jolla, CA). One clone from the ATTS1282 hybridization was designated EL1 and one clone from the ATTS3218

5 hybridization was designated EL2.

A yeast expression library, containing cDNA from *Arabidopsis thaliana* cv. Columbia, was prepared in the lambda YES expression vector described in Elledge et al. (Elledge, S. et al., Proc. Natl. Acad. Sci USA 88:1731-
10 1735 (1991) and was obtained from Ron Davis at Stanford University, Stanford, CA. The library was hybridized with a EL2 partial cDNA probe. A full-length EL2 cDNA was not identified. However, the probe did identify a full-length cDNA which was designated EL3.

15 A consensus sequence for the C-terminal region of EL1, EL2 and the jojoba cDNA polypeptides was identified by sequence alignment using DNA analysis programs from DNASTar, Madison, Wisconsin. This consensus sequence was used to search the *Arabidopsis* EST database again for β -
20 keto acyl synthase sequences. These searches identified four additional putative β -keto acyl synthase ESTs, which were designated EL4 through EL7. EL4, EL5, EL6, and EL7 have homology to Genbank Accession Nos. T04345, T44939, T22193 and T76700, respectively.

25 The lambda YES cDNA expression library described above was hybridized with the EL1 and EL4-EL7 ESTs as probes. This screen identified full-length cDNAs for EL1, EL5 and EL6.

The lambda GEM11 genomic library was hybridized
30 with the EL4 and EL7 ESTs as probes. This screen identified full-length genomic clones for EL4 and EL7. Phage DNA was isolated from each of the hybridizing clones and subcloned into pBluescript as described above.

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The 7 EL clones were sequenced on both strands with regions of overlap for each sequence run.

Sequencing was carried out with an ABI automated sequencer (Applied Biosystems, Inc., Foster City, California), following the manufacturer's instructions.

The nucleotide sequences for the coding regions of EL1-EL7 are shown in Figs. 3, 5, 7, 9, 11, 13 and 15, respectively. The deduced amino acid sequences for EL1-EL7 are shown in Figs. 4, 6, 8, 10, 12, 14 and 16, respectively, using the standard one-letter amino acid code. The EL1, EL2 and EL7 genomic clones appeared to lack introns. The EL4 genomic clone contained one intron near the 5' end of the coding region.

The nucleotide sequences of the 7 EL polynucleotides were compared to 5 DNA sequences present in Genbank. Genbank, National Center for Biotechnology Information, Bethesda, MD. Two of the 5 accessions were cloned from members of the Brassicaceae: the *Arabidopsis* FAE1 sequence (Accession U29142) and a *Brassica napus* sequence (Accession U50771). Three of the accessions were cloned from jojoba (*Simmondsia chinensis*): 2 wax biosynthesis genes (Accessions I14084 and I14085) and a jojoba KAS gene (Accession U37088). See also U.S. Patent 5,445,947, incorporated herein by reference.

Multiple alignment of the 12 sequences was carried out with a computer program sold under the trade name MEGALIGN Lasergene by DNASTar (Madison, Wisconsin). Alignments were done using the Clustal method with weighted residue weight table. The nucleotide sequence similarity index and percent divergence based on the multiple alignment algorithm is shown in Table 1. The nucleotide sequences of EL1-EL7 are distinguishable from the 5 DNA sequences obtained from Genbank.

The deduced amino acid sequences of the EL1-7 polypeptides were compared with the MEGALIGN program to

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the deduced amino acid sequences of the same 5 Genbank clones, using the Clustal method with PAM250 residue weight table. The amino acid sequence similarity and percent divergence are shown in Table 2. The amino acid
5 sequences of EL1-EL7 polypeptides are distinguishable from those of the Genbank sequences.

TABLE 1

Nucleotide sequence pair distances of EL1-EL7, using Clustal method with weighted residue weight table.

	1	2	3	4	5	6	7	8	9	10	11	12	
1		77.5	62.4	58.8	57.0	54.9	47.0	42.8	42.9	43.1	44.7	41.3	1
2	18.1		61.0	57.9	55.4	53.7	46.9	42.7	44.1	42.9	42.3	40.5	2
3	40.4	41.0		70.5	59.3	56.4	46.7	48.5	48.1	48.6	46.5	43.5	3
4	43.9	44.3	28.0		56.3	55.4	46.5	47.0	45.1	47.2	47.4	42.3	4
5	40.7	42.3	45.0	45.0		68.0	54.0	46.8	46.6	46.4	49.0	47.2	5
6	45.8	48.9	46.0	47.3	32.4		53.6	48.6	48.2	48.6	49.0	49.2	6
7	74.1	71.0	69.4	67.3	64.3	64.5		49.8	49.2	49.8	47.7	48.2	7
8	68.1	66.2	63.4	63.1	65.5	64.2	56.1		97.7	99.7	48.4	45.8	8
9	67.0	65.4	63.7	64.6	64.6	64.1	56.6	1.1		95.9	47.6	44.8	9
10	67.2	65.2	61.8	61.4	64.1	63.0	56.3	0.2	1.1		48.4	45.3	10
11	88.6	85.8	81.0	77.0	77.4	82.4	83.1	71.1	71.1	69.9		48.3	11
12	95.7	90.4	95.4	91.5	84.5	82.8	91.9	73.4	73.8	73.3	59.9		12
	1	2	3	4	5	6	7	8	9	10	11	12	

TABLE 2
Amino acid sequence pair distances of EL1-EL7, using Clustal
method with PAM250 residue weight table.

	1	2	3	4	5	6	7	8	9	10	11	12	
1		72.0	62.9	59.8	60.9	60.2	50.3	51.9	52.1	51.5	49.1	42.0	1 EL2
2	31.1		60.1	57.5	58.7	57.1	49.8	49.8	50.0	49.2	49.6	44.4	2 EL3
3	47.4	48.7		82.4	60.7	63.0	50.0	51.4	51.6	50.8	47.8	43.9	3 ATPAE1 U29142
4	51.8	52.8	17.9		60.2	61.0	49.2	50.3	50.5	49.7	46.5	42.4	4 BNFAB1 U50771
5	49.0	51.3	45.8	46.2		75.8	61.0	58.7	58.9	58.3	55.0	55.6	5 EL7
6	52.6	55.5	42.8	46.5	29.3		61.8	55.7	55.7	54.9	52.9	50.5	6 EL5
7	74.7	70.5	71.8	74.4	52.0	50.8		52.8	52.8	51.8	53.4	51.6	7 EL6
8	66.7	69.2	66.2	67.3	54.8	59.8	67.7		99.8	96.9	53.1	52.0	8 JOJKCS U37088
9	66.3	68.7	66.2	67.3	54.0	59.3	67.7	0.2		96.9	53.1	51.9	9 JKCS11 I14085
10	66.3	69.7	66.6	67.8	54.5	60.7	68.6	1.8	1.6		51.7	50.7	10 JKCS10 I14084
11	73.6	73.7	72.8	74.4	60.8	66.0	67.2	63.9	63.9	65.3		50.8	11 EL1
12	84.8	85.5	82.7	83.3	60.6	70.8	67.1	68.5	68.5	69.9	69.4		12 EL4
	1	2	3	4	5	6	7	8	9	10	11	12	

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Example 4

Expression of EL1 and EL2 in Yeast

The open reading frames (ORFs) for the EL2, EL4 and EL7 clones were amplified by PCR. The EL2 ORF was cloned into λ YES using the primers: CTCGAGCAAGTCCACTACCACGCA and CTCGAGCGAGTCAGAAGGAACAAA. The EL4 ORF was cloned into pYEura3 using the primers: GATAATTTAGAGAGGCACAGGGT and GTCGACACAAGAATGGGTAGATCCAA. The EL7 ORF was cloned into pYEura3 using the primers: CAGTTCCTCAAACGAAGCTA and GTCGACTTCTCAATGGACGGTGCCGGA. Amplified products were cloned into pYEura3 under the control of, and 3' to, the GAL1 promoter. The resulting plasmids were transformed into yeast as described in Example 1.

Yeast cultures containing full-length EL1 in λ YES and full-length EL2 in pYEura3 were grown in the presence of galactose or glucose as described in Example 2. Microsomes were then prepared from each of the cultures and fatty acid elongation assays were carried out as described in Example 2.

In the first experiment, microsomes were prepared from galactose-induced cultures of EL1, EL2 and FAE1, and incubated with either [1- 14 C] 18:0 acyl-CoA or [1- 14 C] 18:1 acyl-CoA as substrate. The amounts of various reaction products synthesized after 30 minutes (min) were determined as described in Example 2. The results when 18:0 acyl-CoA was the substrate are shown in Table 3. The results when 18:1 acyl-CoA was the substrate are shown in Table 4.

Table 3.
Elongation of 18:0-CoA by FAE1, EL1 and EL2 Genes
Expressed in Yeast

β -Keto Acyl Synthase Gene						
Acyl-CoA Product	FAE1		EL1		EL2	
	Rate ¹	(%)	Rate	(%)	Rate	(%)
20:0	0.369	64.3	0.084	38.8	0.108	41.8
22:0	0.113	18.6	0.047	21.9	0.053	20.7
24:0	0.065	10.7	0.043	19.9	0.052	20.3
26:0	0.038	6.3	0.042	19.4	0.044	17.2
Total	0.585	100.0	0.216	100.0	0.258	100.0

¹ Nanomoles/minute/mg of microsomal protein

- 29/A -

Table 4.
Elongation of 18:1-CoA by FAE1, EL1 and EL2 Genes
Expressed in Yeast

β -Keto Acyl Synthase Gene						
Acyl-CoA Product	FAE1		EL1		EL2	
	Rate ¹	(%)	Rate	(%)	Rate	(%)
20:1	1.131	84.6	0.111	80.8	0.091	84.1
22:1	0.206	15.4	0.026	19.2	0.017	15.9
24:1	0.0	0.0	0.0	0.0	0.0	0.0
26:1	0.0	0.0	0.0	0.0	0.0	0.0
Total	1.337	100.0	0.137	100.0	0.108	100.0

¹ Nanomoles/minute/mg of microsomal protein

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The results shown in Tables 3 and 4 indicate that the EL1 and EL2 gene products have β -ketoacyl synthase (KAS) activity and that the KAS reaction product can be utilized to form VLCFAs. The specific activities of the 3 KAS enzymes cannot be compared, since the relative amount of the heterologous KAS protein in each microsomal preparation is not known. However, the proportions of various reaction products can be compared between FAE1, EL1 and EL2.

The data shown in Table 3 indicate that the EL1 and EL2 KAS activities result in a higher proportion of saturated VLCFAs than does the FAE1 KAS activity. These

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results suggest that EL1 and EL2 encode novel gene products, because EL1 and EL2 have a greater preference for C22:0 and C24:0 acyl-CoA substrates than does FAE1.

A comparison of the relative elongation activity of FAE1 with 18:0 and 18:1 substrates (Tables 3 and 4) indicates that FAE1 is more active when 18:1 is the substrate than when 18:0 is the substrate. In contrast, the overall rate of product formation with EL1 is less when 18:1 is the substrate than when 18:0 is the substrate (Tables 3 and 4). EL2 is also less active when 18:1 is the substrate than when 18:0 is the substrate (Tables 3 and 4). These results support the conclusion that EL1 and EL2 encode novel gene products and suggest that EL1 and EL2 have a preference for saturated fatty acids as substrates, whereas the FAE1 gene product has a preference for monounsaturated fatty acids as substrates.

In a second experiment, microsomes were prepared from galactose-induced and from glucose-repressed yeast cultures containing EL1 or EL2 coding sequences. The microsomal preparations were incubated with either 18:0 acyl-CoA or 18:1 acyl-CoA as substrate and the fatty acid reaction products determined as described above. The results with the 18:0 substrate are shown in Table 5. The results with the 18:1 substrate are shown in Table 6.

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Table 5.
Elongation of 18:0-CoA by EL1 and EL2
With and Without Induction of Gene Expression

Acyl CoA	S-Keto Acyl Synthase Gene							
	EL1				EL2			
	+Glucose		+Galactose		+Glucose		+Galactose	
	Rate ¹	(%)	Rate	(%)	Rate	(%)	Rate	(%)
20:0	0.007	100.0	0.074	55.8	0.030	81.3	0.107	43.1
22:0	0.000	0.0	0.023	17.4	0.002	5.1	0.044	17.8
24:0	0.000	0.0	0.020	15.3	0.005	13.6	0.048	19.1
26:0	0.000	0.0	0.015	11.5	0.000	0.0	0.050	20.0
Total	0.007	100.0	0.133	100.0	0.037	100.0	0.249	100.0

¹ Nanomoles/minute/mg of microsomal protein

Table 6.
Elongation of 18:1-CoA by EL1 and EL2
With and Without Induction of Gene Expression

Acyl CoA	S-Keto Acyl Synthase Gene							
	EL1				EL2			
	+Glucose		+Galactose		+Glucose		+Galactose	
	Rate ¹	(%)	Rate	(%)	Rate	(%)	Rate	(%)
20:1	0.062	100.0	0.081	100.0	0.043	100.0	0.089	100.0
22:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
24:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
26:1	0.000	0.0	0.000	0.0	0.000	0.0	0.000	0.0
Total	0.062	100.0	0.081	100.0	0.043	100.0	0.089	100.0

¹ Nanomoles/minute/mg of microsomal protein

The results in Table 5 show *in vitro* elongase activity for EL1 and EL2 under induced (galactose) and uninduced (glucose) conditions. The comparison indicates that induction with galactose results in a large increase in overall elongase activity when 18:0 acyl CoA is the substrate (about 19-fold and 7-fold for EL1 and EL2, respectively). In contrast, induction when 18:1 acyl CoA is the substrate results in only a small increase in elongase activity (about 1.3-fold and 2-fold for EL1 and EL2, respectively), as shown in Table 6.

The results in Table 5 show that little or no VLCFA products are made by yeast microsomes under uninduced conditions. Upon induction of EL1 and EL2 gene

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expression, however, significant quantities of C20:0, C22:0, C24:0 and C26:0 are made. The data in Tables 5 and 6 are consistent with the results in Tables 3 and 4, which indicated that EL1 and EL2 were more active with a saturated fatty acid substrate than with a monounsaturated substrate.

The data in Tables 5 and 6 are also consistent with the data in Tables 3 and 4 indicating that the EL1 and EL2 gene products are more active in converting C24:0 to C26:0 than is *FAE1*.

In a third experiment, microsomes from induced and uninduced cultures containing EL1 or EL2 were incubated in the absence of cofactors involved in the β -ketoacyl condensation reaction. Cultures were induced and microsomes were prepared as described in Example 2. *In vitro* assays were carried out as described in Example 2, except that either ATP, CoASH or both were omitted from the enzyme reaction mixture. In addition, one reaction was carried out in a complete mixture having 0.01 mM of cerulenin (Sigma, St. Louis, MO). Cerulenin is an inhibitor of some condensing enzymes. The results are shown in Tables 7-9.

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Table 7.
Effect of Cofactors on 18:0-CoA Elongation¹

Gene	Expt ⁴	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+ Cer ³
EL1	1	.037	.109	.095	.105	.119	.141
	2	N.D.	.090	.125	.093	.270	.176
EL2	1	.033	.112	.168	.127	.143	.238
	2	N.D.	.120	.178	.133	.195	.302

¹ Activity in nanomoles/minute/mg of microsomal protein.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

⁴ Experiment No.

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Table 8.
Effect of Cofactors on Elongation Products of EL1¹

Prod.	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+Cer ³
20:0	53.9	46.2	34.4	47.8	41.7	46.7
22:0	14.4	18.7	13.7	18.0	19.4	16.2
24:0	18.5	18.1	20.6	19.1	16.7	17.7
26:0	13.2	17.1	31.4	15.2	22.3	19.4
Total	100.0	100.0	100.0	100.0	100.0	100.0

¹ Amount of indicated product as a percent of total products formed. Results of one experiment for +Glucose; Average of two experiments for other conditions.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

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Table 9.
Effect of Cofactors on Elongation Products of EL2¹

Prod.	+Glu ²	+Gal ²	-ATP ³	-CoA ³	-A&C ³	+Cer ³
20:0	54.5	47.1	34.1	45.3	38.0	41.8
22:0	17.1	19.1	16.4	19.2	15.9	16.1
24:0	5.8	19.4	20.8	19.9	18.4	20.4
26:0	22.6	14.5	28.9	15.8	27.8	21.8
Total	100.0	100.0	100.0	100.0	100.0	100.0

¹ Amount of indicated product as a percent of total products formed. Results of one experiment for +Glucose; Average of two experiments for other conditions.

² +Glu: microsomes from cultures grown in the presence of glucose and incubated in standard reaction mix; +Gal: microsomes from cultures grown in the presence of galactose and incubated in standard reaction mix.

³ Microsomes from galactose-induced cultures. -ATP: ATP omitted from reaction mix; -CoA: Coenzyme A omitted from reaction mix; -A&C: ATP and Coenzyme A omitted from reaction mix; +Cer: Standard reaction mix containing 0.01 mM cerulenin.

The results in Table 7 indicate that omission of ATP and/or CoA from the incubation mixture does not have a significant effect on the overall amounts of VLCFAs synthesized by the *in vitro* KAS activity of EL1 or EL2. The results also show that cerulenin does not inhibit the KAS activity of EL1 or EL2. The data in Table 8 and 9 confirm that EL1 and EL2 KAS activity produces significant amounts of C24:0 and C26:0 acyl CoA products.

To the extent not already indicated, it will be understood by those of ordinary skill in the art that any one of the various specific embodiments herein described and illustrated may be further modified to incorporate features shown in other of the specific embodiments.

The foregoing detailed description has been provided for a better understanding of the invention only and no unnecessary limitation should be understood therefrom as some modifications will be apparent to those

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skilled in the art without deviating from the spirit and scope of the appended claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: CARGILL, INCORPORATED
- (ii) TITLE OF THE INVENTION: FATTY ACID ELONGASES
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/868,373
 - (B) FILING DATE: 03-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lundquist, Ronald C
 - (B) REGISTRATION NUMBER: 37,875
 - (C) REFERENCE/DOCKET NUMBER: 07039/064W01
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-335-5050
 - (B) TELEFAX: 612-288-9696
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGATCGAG	AGAGATTAAAC	GGCGGAGATG	GCGTTTCGAG	ATTCATCATC	GGCCGTTATA	60
AGAAITCGAA	GACGTTTGCC	GGATTTATTA	ACGTCCGTTA	AGCTCAAATA	CGTGAAGCTT	120
GGACTTCACA	ACTCTTGCAA	CGTGACCACC	ATTCTCTTCT	TCTTAATTAT	TCTTCCTTTA	180
ACCGGAACCG	TGCTGGTTCA	GCTAACCGGT	CTAACGTTTCG	ATACGTTCTC	TGAGCTTTGG	240
TCTAACCAGG	CGGTTCAACT	CGACACGGCG	ACGAGACTTA	CCTGCTTGGT	TTTCCTCTCC	300
TTTCGTTTTGA	CCCTCTACGT	GGCTAACC GG	TCTAAACCGG	TTTACCTAGT	GGATTTCTCC	360
TGCTACAAAC	CGGAAGACGA	GCGTAAATA	TCAGTAGATT	CGTTCTTGAC	GATGACTGAG	420
GAAAATGGAT	CATTCACCGA	TGACACGGTT	CAGTTCCAGC	AAAGAATCTC	GAACCGGGCC	480

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GGTTTGGGAG ACAGAGACGTA TCTGCCACGT GGCATAACTT CAACGCCCCC GAAGCTAAAT 540
ATGTCAGAGG CACGTGCCGA AGCTGAAGCC GTTATGTTTG GAGCCTTAGA TTCCCTCTTC 600
GAGAAAACCG GAATTAAACC GGCCGAAGTC GGAATCTTGA TAGTAAACTG CAGCTTATTC 660
AATCCGACGC CGTCTCTATC AGCGATGATC GTGAACCATT ACAAGATGAG AGAAGACATC 720
AAAAGTTACA ACCTCGGAGG AATGGGTTGC TCCGCCGGAT TAATCTCAAT CGATCTCGCT 780
AACAACTCTCC TCAAAGCAAA CCCTAATTCT TACGCTGTCG TGGTAAGCAC GGAAAACATA 840
ACCCTAAACT GGTACTTCGG AAATGACCGG TCAATGCTCC TCTGCAACTG CATCTTCCGA 900
ATGGGCGGAG CTGCGATTCT CCTCTCTAAC CGCCGTCAAG ACCGGAAGAA GTCAAAGTAC 960
TCGCTGGTCA ACGTCGTTTC AACACATAAA GGATCAGACG ACAAGAACTA CAATTGCGTG 1020
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GTCGCCGGAG ACGCTCTGAA AACAAACATC ACGACTTTAG GACCGATGGT TCTTCCATTG 1140
TCAGAGCAGT TGATGTTCTT GATTTCCTTG GTCAAAAGGA AGATGTTCAA GTTAAAAGTT 1200
AAACCGTATA TTCCGGATTT CAAGCTAGCT TTCGAGCATT TCTGTATTCA CGCAGGAGGT 1260
AGAGCGGTTT TAGACGAAGT GCAGAAGAAT CTTGATCTCA AAGATTGGCA CATGGAACCT 1320
TCTAGAATGA CTTTGCACAG ATTTGGTAAC ACTTCGAGTA GCTCGCTTTG GTATGAGATG 1380
GCTTATACCG AAGCTAAGGG TCGGGTTAAA GCTGGTGACC GACTTTGGCA GATTGCGTTT 1440
GGATCGGGTT TCAAGTGTA TAGTGCGGTT TGGAAAGCGT TACGACCGGT TTCGACGGAG 1500
GAGATGACCG GTAATGCTTG GGCTGGTTTC ATTGATCAAT ATCCGGTTAA AGTTGTGCAA 1560

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Ser Ala Val Ile Arg Ile Arg Arg Arg Leu Pro Asp Leu Leu Thr Ser
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Val Lys Leu Lys Tyr Val Lys Leu Gly Leu His Asn Ser Cys Asn Val
          35          40          45
Thr Thr Ile Leu Phe Phe Leu Ile Ile Leu Pro Leu Thr Gly Thr Val
          50          55          60
Leu Val Gln Leu Thr Gly Leu Thr Phe Asp Thr Phe Ser Glu Leu Trp
          65          70          75          80
Ser Asn Gln Ala Val Gln Leu Asp Thr Ala Thr Arg Leu Thr Cys Leu
          85          90          95
Val Phe Leu Ser Phe Val Leu Thr Leu Tyr Val Ala Asn Arg Ser Lys
          100          105          110
Pro Val Tyr Leu Val Asp Phe Ser Cys Tyr Lys Pro Glu Asp Glu Arg
          115          120          125
Lys Ile Ser Val Asp Ser Phe Leu Thr Met Thr Glu Asn Gly Ser
          130          135          140
Phe Thr Asp Asp Thr Val Gln Phe Gln Gln Arg Ile Ser Asn Arg Ala
          145          150          155          160
Gly Leu Gly Asp Glu Thr Tyr Leu Pro Arg Gly Ile Thr Ser Thr Pro
          165          170          175
Pro Lys Leu Asn Met Ser Glu Ala Arg Ala Glu Ala Glu Ala Val Met
          180          185          190
Phe Gly Ala Leu Asp Ser Leu Phe Glu Lys Thr Gly Ile Lys Pro Ala
          195          200          205
Glu Val Gly Ile Leu Ile Val Asn Cys Ser Leu Phe Asn Pro Thr Pro
          210          215          220
Ser Leu Ser Ala Met Ile Val Asn His Tyr Lys Met Arg Glu Asp Ile
          225          230          235          240
Lys Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser
          245          250          255
Ile Asp Leu Ala Asn Asn Leu Leu Lys Ala Asn Pro Asn Ser Tyr Ala
          260          265          270
Val Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Phe Gly Asn
          275          280          285

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Asp	Arg	Ser	Met	Leu	Leu	Cys	Asn	Cys	Ile	Phe	Arg	Met	Gly	Gly	Ala	
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Ala	Ile	Leu	Leu	Ser	Asn	Arg	Arg	Gln	Asp	Arg	Lys	Lys	Ser	Lys	Tyr	
305					310					315					320	
Ser	Leu	Val	Asn	Val	Val	Arg	Thr	His	Lys	Gly	Ser	Asp	Asp	Lys	Asn	
			325						330					335		
Tyr	Asn	Cys	Val	Tyr	Gln	Lys	Glu	Asp	Glu	Arg	Gly	Thr	Ile	Gly	Val	
			340					345					350			
Ser	Leu	Ala	Arg	Glu	Leu	Met	Ser	Val	Ala	Gly	Asp	Ala	Leu	Lys	Thr	
		355					360					365				
Asn	Ile	Thr	Thr	Leu	Gly	Pro	Met	Val	Leu	Pro	Leu	Ser	Glu	Gln	Leu	
370						375					380					
Met	Phe	Leu	Ile	Ser	Leu	Val	Lys	Arg	Lys	Met	Phe	Lys	Leu	Lys	Val	
385					390					395					400	
Lys	Pro	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	Ile	
			405						410					415		
His	Ala	Gly	Gly	Arg	Ala	Val	Leu	Asp	Glu	Val	Gln	Lys	Asn	Leu	Asp	
		420						425					430			
Leu	Lys	Asp	Trp	His	Met	Glu	Pro	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	
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Gly	Asn	Thr	Ser	Ser	Ser	Ser	Leu	Trp	Tyr	Glu	Met	Ala	Tyr	Thr	Glu	
450						455					460					
Ala	Lys	Gly	Arg	Val	Lys	Ala	Gly	Asp	Arg	Leu	Trp	Gln	Ile	Ala	Phe	
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Val	Ser	Thr	Glu	Glu	Met	Thr	Gly	Asn	Ala	Trp	Ala	Gly	Ser	Ile	Asp	
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		515					520									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTACC	CCATGAAGAA	GGTAAAAATC	TTTTTCAACT	ACCTCATGGC	GCATCGCTTC	60
AAGCTCTGCT	TCTTACCATT	AATGGTTGCT	ATAGCCGTGG	AGGCGTCTCG	TCTTTCCACA	120
CAAGATCTCC	AAAACCTTTA	CCTCTACTTA	CAAAACAACC	ACACATCTCT	AACCATGTTT	180
TTCCCTTACC	TCGCTCTCGG	GTCGACTCTT	TAACTCATGA	CCCGGCCCAA	ACCCGTTTAT	240
CTCGTTGACT	TTAGCTGCTA	CCTCCACCG	TCGCATCTCA	AAGCCAGCAC	CCAGAGGATC	300
ATGCAACACG	TAAGGCTTGT	ACGAGAAGCA	GGCGCGTGGA	AGCAAGAGTC	CGATTACTTG	360
ATGGACTTCT	GCGAGAAGAT	TCTAGAACGT	TCCGGTCTAG	GCCAAGAGAC	GTACGTACCC	420
GAAGGTCTTC	AAACTTTGCC	ACTACAACAG	AATTTGGCTG	TATCACGTAT	AGAGACGGAG	480
GAAGTTATTA	TTGGTGCGGT	CGATAATCTG	TTTCGCAACA	CGGGAATAAG	CCCTAGTGAT	540
ATAGGTATAT	TGGTGGTGAA	TTCAAGCACT	TTTAATCCAA	CACCTTCGCT	ATCAAGTATC	600
TTAGTGAATA	AGTTTAAACT	TAGGGATAAT	ATAAAGAGCT	TGAATCTTGG	TGGGATGGGG	660
TGTAGCGCTG	GAGTCATCGC	TATCGATGCG	GCTAAGAGCT	TGTTACAAGT	TCATAGAAAC	720
ACTTATGCTC	TTGTGGTGAG	CACGGAGAAC	ATCACTCAAA	ACTTGTACAT	CGGTAACAAC	780
AAATCAATGT	TGGTTACAAA	CTGTTTGTTT	CGTATAGGTG	GGGCCGCGAT	TTTGCTTTCT	840
AACCGGTCTA	TAGATCGTAA	ACGCGCAAAA	TACGAGCTTG	TTACACCCGT	GCGGGTCCAT	900
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GCATTTCGAGC	ATTTCTGTAT	CCATGCGGGT	GGTAGAGCGC	TAATTGATGA	GATGGAGAAG	1200
AATCTTCATC	TAACTCCACT	AGACGTTGAG	GCTTCAAGAA	TGACATTACA	CAGGTTTGGT	1260
AATACCTCTT	CGAGCTCCAT	TTGGTACGAG	TTGGCTTACA	CAGAAGCCAA	AGGAAGGATG	1320
ACGAAAGGAG	ATAGGATTTG	GCAGATTGCG	TTGGGGTCAG	GTTTTAAGTG	TAATAGTTCA	1380

- 40 -

GTTTGGGTGG CTCTTCGTAA CGTCAAGCCT TCTACTAATA ATCCTTGGGA ACAGTGCTCA 1440
 CACAAATATC CAGTTGAGAT CGATATAGAT TTAAGAGAG 1479

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Val	Glu	Ala	Ser	Arg	Leu	Ser	Thr	Gln	Asp	Leu	Gln	Asn	Phe	Tyr	Leu	40	45	50	55
Tyr	Leu	Gln	Asn	Asn	His	Thr	Ser	Leu	Thr	Met	Phe	Phe	Leu	Tyr	Leu	60	65	70	75
Ala	Leu	Gly	Ser	Thr	Leu	Tyr	Leu	Met	Thr	Arg	Pro	Lys	Pro	Val	Tyr	80	85	90	95
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Thr	Gln	Arg	Ile	Met	Gln	His	Val	Arg	Leu	Val	Arg	Glu	Ala	Gly	Ala	120	125	130	135
Trp	Lys	Gln	Glu	Ser	Asp	Tyr	Leu	Met	Asp	Phe	Cys	Glu	Lys	Ile	Leu	140	145	150	155
Glu	Arg	Ser	Gly	Leu	Gly	Gln	Glu	Thr	Tyr	Val	Pro	Glu	Gly	Leu	Gln	160	165	170	175
Thr	Leu	Pro	Leu	Gln	Gln	Asn	Leu	Ala	Val	Ser	Arg	Ile	Glu	Thr	Glu	180	185	190	195
Glu	Val	Ile	Ile	Gly	Ala	Val	Asp	Asn	Leu	Phe	Arg	Asn	Thr	Gly	Ile	200	205	210	215
Ser	Pro	Ser	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Thr	Phe	Asn	220	225	230	235
Pro	Thr	Pro	Ser	Leu	Ser	Ser	Ile	Leu	Val	Asn	Lys	Phe	Lys	Leu	Arg	240	245	250	255
Asp	Asn	Ile	Lys	Ser	Leu	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	260	265	270	275
Val	Ile	Ala	Ile	Asp	Ala	Lys	Ser	Leu	Leu	Gln	Val	His	Arg	Asn		280	285	290	295
Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn	Leu	Tyr	300	305	310	315
Met	Gly	Asn	Asn	Lys	Ser	Met	Leu	Val	Thr	Asn	Cys	Leu	Phe	Arg	Ile	320	325	330	335
Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Arg	Ser	Ile	Asp	Arg	Lys	Arg	340	345	350	355
Ala	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Val	His	Thr	Gly	Ala	Asp	360	365	370	375
Asp	Arg	Ser	Tyr	Glu	Cys	Ala	Thr	Gln	Glu	Glu	Asp	Glu	Asp	Gly	Ile	380	385	390	395
Val	Gly	Val	Ser	Leu	Ser	Lys	Asn	Leu	Pro	Met	Val	Ala	Ala	Arg	Thr	400	405	410	415
Leu	Lys	Ile	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Ile	Ser				
Glu	Lys	Phe	His	Phe	Phe	Val	Arg	Phe	Val	Lys	Lys	Lys	Phe	Leu	Asn				
Pro	Lys	Leu	Lys	His	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Glu	His				
Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Leu	Ile	Asp	Glu	Met	Glu	Lys				
Asn	Leu	His	Leu	Thr	Pro	Leu	Asp	Val	Glu	Ala	Ser	Arg	Met	Thr	Leu				

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His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala
 420 425 430
 Tyr Thr Glu Ala Lys Gly Arg Met Thr Lys Gly Asp Arg Ile Trp Gln
 435 440 445
 Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ser Val Trp Val Ala
 450 455 460
 Leu Arg Asn Val Lys Pro Ser Thr Asn Asn Pro Trp Glu Gln Cys Leu
 465 470 475 480
 His Lys Tyr Pro Val Glu Ile Asp Ile Asp Leu Lys Glu
 485 490

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

CTACGTCAGG GTAGAACAAA GAGTAAACAC TTAAGCAAAA CAATTTGTCC TACTCTTAGG      60
TTATCTCCAA TGAAGAACTT AAAGATGGTT TTCTTCAAGA TCCTCTTTAT CTCTTTAATG      120
GCAGGATTAG CCATGAAAGG ATCTAAGATC AACGTAGAAG ATCTCCAAAA GTTCTCCCTC      180
CACCATAACAC AGAACAACCT CCAAACCATA AGCCTTCTAT TGTTCCTTGT CGTTTTTGTG      240
TGGATCCTCT ACATGTTAAC CCGACCTAAA CCCGTTTACC TTGTTGATTT CTCCTGCTAC      300
CTTCCACCGT CGCATCTCAA GGTCAGTATC CAAACCCTAA TGGGACACGC AAGACGTGCA      360
AGAGAAGCAG GCATGTGTTG GAAGAACAAA GAGAGCGACC ATTAGTTGA CTTCCAGGAG      420
AAGATTCTTG AACGTTCCGG TCTTGGTCAA GAAACCTACA TCCCGAGGG TCTTCAGTGC      480
TTCCCACCTC AGCAAGGCAT GGGTGCTTCA CGTAAAGAGA CGGAAGAAGT AATCTTCGGA      540
GCTCTTGACA ATCTTTTTCG CAACACCGGT GTAAACCTG ATGATATCGG TATATTGGTG      600
GTGAATTCTA GCACGTTTAA TCCAACCTCA TCACTCGCCT CCATGATTGT GAACAAGTAC      660
AAACTCAGAG ACAACATCAA GAGTTTGAAT CTTGGAGGGA TGGGTTGCAG TGCCGGAGTT      720
ATAGCTGTTG ATGTCGCTAA GGGATTACTA CAAGTTCATA GGAACACTTA TGCTATTGTA      780
GTAAGCACAG AGAACATCAC TCAGAACTTA TACTTGGGGA AAAACAAATC AATGCTAGTC      840
ACAAACTGTT TGTTCGCGT TGGTGGTGCT GCGGTTCTGC TTTCAAACAG ATCTAGAGAC      900
CGTAACCGCG CCAAATACGA GCTTGTTTAC ACCGTACGGA TCCATACCGG ATCAGATGAT      960
AGGTCGTTCT AATGTGCGAC ACAAGAAGAG GATGAAGATG GTATAATTGG AGTTACCTTG      1020
ACAAAGAATC TACCTATGGT GGCTGCAAGG ACTCTTAAGA TAAATATCGC AACTTTGGGT      1080
CCTCTTGTA TCCATTAAA AGAGAAGCTA GCCTTCTTTA TTACTTTTGT CAAGAAGAAG      1140
TATTTCAAGC CAGAGTTAAG GAATTATACA CCAGATTTC AAGCTTGCTT TGAGCATTTT      1200
TGTATCCACG CTGGTGGAAG AGCTCTAATA GATGAGCTGG AGAAGAACCT TAAGCTTTCT      1260
CCGTACACG TAGAGGCGTC AAGAATGACA CTACACAGGT TTGGTAACAC TTCTTCTAGC      1320
TCAATCTGGT ACGAGTTAGC TTATACAGAA GCTAAAGGAA GGATGAAGGA AGGAGATAGG      1380
ATTTGGCAGA TTGCTTTGGG GTCAGGTTTT AAGTGTAACA GTTCAGTATG GGTGGCTCTG      1440
CGAGACGTTA AGCCTTCAGC TAACAGTCCA TGGGAAGACT GTATGGATAG ATATCCGGTT      1500
GAGATTGATA TT

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Arg Gln Gly Arg Thr Lys Ser Lys His Leu Ser Lys Thr Ile Cys
 1 5 10 15
 Pro Thr Leu Arg Leu Ser Pro Met Lys Asn Leu Lys Met Val Phe Phe
 20 25 30

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Lys Ile Leu Phe Ile Ser Leu Met Ala Gly Leu Ala Met Lys Gly Ser
 35 40 45
 Lys Ile Asn Val Glu Asp Leu Gln Lys Phe Ser Leu His His Thr Gln
 50 55 60
 Asn Asn Leu Gln Thr Ile Ser Leu Leu Leu Phe Leu Val Val Phe Val
 65 70 75 80
 Trp Ile Leu Tyr Met Leu Thr Arg Pro Lys Pro Val Tyr Leu Val Asp
 85 90 95
 Phe Ser Cys Tyr Leu Pro Pro Ser His Leu Lys Val Ser Ile Gln Thr
 100 105 110
 Leu Met Gly His Ala Arg Arg Ala Arg Glu Ala Gly Met Cys Trp Lys
 115 120 125
 Asn Lys Glu Ser Asp His Leu Val Asp Phe Gln Glu Lys Ile Leu Glu
 130 135 140
 Arg Ser Gly Leu Gly Gln Glu Thr Tyr Ile Pro Glu Gly Leu Gln Cys
 145 150 155 160
 Phe Pro Leu Gln Gln Gly Met Gly Ala Ser Arg Lys Glu Thr Glu Glu
 165 170 175
 Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Arg Asn Thr Gly Val Lys
 180 185 190
 Pro Asp Asp Ile Gly Ile Leu Val Val Asn Ser Ser Thr Phe Asn Pro
 195 200 205
 Thr Pro Ser Leu Ala Ser Met Ile Val Asn Lys Tyr Lys Leu Arg Asp
 210 215 220
 Asn Ile Lys Ser Leu Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val
 225 230 235 240
 Ile Ala Val Asp Val Ala Lys Gly Leu Leu Gln Val His Arg Asn Thr
 245 250 255
 Tyr Ala Ile Val Val Ser Thr Glu Asn Ile Thr Gln Asn Leu Tyr Leu
 260 265 270
 Gly Lys Asn Lys Ser Met Leu Val Thr Asn Cys Leu Phe Arg Val Gly
 275 280 285
 Gly Ala Ala Val Leu Leu Ser Asn Arg Ser Arg Asp Arg Asn Arg Ala
 290 295 300
 Lys Tyr Glu Leu Val His Thr Val Arg Ile His Thr Gly Ser Asp Asp
 305 310 315 320
 Arg Ser Phe Glu Cys Ala Thr Gln Glu Glu Asp Glu Asp Gly Ile Ile
 325 330 335
 Gly Val Thr Leu Thr Lys Asn Leu Pro Met Val Ala Ala Arg Thr Leu
 340 345 350
 Lys Ile Asn Ile Ala Thr Leu Gly Pro Leu Val Leu Pro Leu Lys Glu
 355 360 365
 Lys Leu Ala Phe Phe Ile Thr Phe Val Lys Lys Lys Tyr Phe Lys Pro
 370 375 380
 Glu Leu Arg Asn Tyr Thr Pro Asp Phe Lys Leu Ala Phe Glu His Phe
 385 390 395 400
 Cys Ile His Ala Gly Gly Arg Ala Leu Ile Asp Glu Leu Glu Lys Asn
 405 410 415
 Leu Lys Leu Ser Pro Leu His Val Glu Ala Ser Arg Met Thr Leu His
 420 425 430
 Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr
 435 440 445
 Thr Glu Ala Lys Gly Arg Met Lys Glu Gly Asp Arg Ile Trp Gln Ile
 450 455 460
 Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ser Val Trp Val Ala Leu
 465 470 475 480
 Arg Asp Val Lys Pro Ser Ala Asn Ser Pro Trp Glu Asp Cys Met Asp
 485 490 495
 Arg Tyr Pro Val Glu Ile Asp Ile
 500

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

ATGGGTTAGAT CCAACGAGCA AGATCTGCTC TCTACCGAGA TCGTTAATCG TGGGATCGAA      60
CCATCCGGTTC CTAACGCCGG CTCACCAACG TTCTCGGTTA GGGTCAGGAG ACGTTTGCCT      120
GATTTTCTTTC AGTCGGTGAA CTTGAAGTAC GTGAAACTTG GTTACCACTA CCTCATAAAC      180
CATGCGGTTT ATTTGGCGAC CATACCGGTT CTTGTGCTGG TTTTGTAGTC TGAGGTTGGG      240
AGTTTAAGCA GAGAAGAGAT TTGGAAGAAG CTTTGGGACT ATGATCTTGC AACTGTTATC      300
GGATTCCTTCG GTGTCTTTGT TTTAACCGCT TGTGTCTACT TCATGTCTCG TCCTCGCTCT      360
GTTTATCTTA TTGATTTTCG TGTTTACAAG CCTCCGATG AACACAAGGT GACAAAAGAA      420
GAGTTCATAG AACTAGCGAG AAAATCAGGG AAGTTCGACG AAGAGACACT CGGTTTCAAG      480
AAGAGGATCT TACAAGCCTC AGGCATAGCG GACGAGACAT ACGTCCCAAG ATCCATCTCT      540
TCATCAGAAA ACATAACAAC GATGAAAGAA GGTCTGTAAG AAGCCTCTAC AGTGATCTTT      600
GGAGCACTAG ACGAACTCTT CGAGAAGACA CGTGTAAGAA CTAAAGACGT TGGTGTCTCT      660
GTGGTTAACT GTAGCATTTT CAACCCGACA CCGTCGTTGT CCGCAATGGT GATAAACCAT      720
TACAAGATGA GAGGGAACAT ACTTAGTTAC AACCTTGGAG GGATGGGATG TTCGGCTGGA      780
ATCATAGCTA TTGATCTTGC TCGTGACATG CTTTCAGTCTA ACCCTAATAG TTATGCTGTT      840
GTTGTGAGTA CTGAGATGGT TGGGTATAAT TGGTACGTGG GAAGTGACAA GTCAATGGTT      900
ATACCTAATT GTTTCTTTAG GATGGGTTGT TCTGCCGTTA TGCTCTCTAA CCGTCGCTCGT      960
GACTTTCGCC ATGCTAAGTA CCGTCTCGAG CACATTGTCC GAACTCATAA GGCTGCTGAC      1020
GACCGTAGCT TCAGGAGTGT GTACCAGGAA GAAGATGAAC AAGGATTCAA GGGGTTGAAG      1080
ATAAGTAGAG ACTTAATGGA AGTTGGAGGT GAAGCTCTCA AGACAAACAT CACTACCTTA      1140
GGTCCTCTTG TCCTACCTTT CTCCGAGCAG CTTCTCTTCT TTGCTGCTTT GGTCCGCCGA      1200
ACATTCTCAC CTGCTGCCAA AACGTCCACA ACCACTTCCT TCTCTACTTC CGCCACCGCA      1260
AAAACCAATG GAATCAAGTC TTCCTCTTCC GATCTGTCCA AGCCATACAT CCCGACTAC      1320
AAGCTCGCCT TCGAGCATTT TTGCTTCCAC GCGGCAAGCA AAGTAGTGCT TGAAGAGCTT      1380
CAAAGAATC TAGGCTTGAG TGAAGAGAA ATGGAGGCTT CTAGGATGAC ACTTCACAGG      1440
TTTGGAAACA CTTCTAGCAG TGAATCTGG TATGAGTTGG CTTACATGGA GGCCAAGGAA      1500
AGTGTTCGTA GAGGCGATAG GGTTTGGCAG ATCGCTTTCG GTTCTGGTTT TAAGTGTAAC      1560
AGTGTGGTGT GGAAGGCAAT GAGGAAGGTG AAGAAGCCAA CCAGGAACAA TCCTTGGGTG      1620
GATTGCATCA ACCGTTACCC TGTGCCTCTC

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Gly Arg Ser Asn Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn
 1           5           10           15
Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser
 20           25           30
Val Arg Val Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu
 35           40           45
Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr
 50           55           60
Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly
 65           70           75           80
Ser Leu Ser Arg Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Leu
 85           90           95
Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Ala Cys Val
100           105           110

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Tyr	Phe	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Ile	Asp	Phe	Ala	Cys
		115					120					125			
Tyr	Lys	Pro	Ser	Asp	Glu	His	Lys	Val	Thr	Lys	Glu	Glu	Phe	Ile	Glu
	130					135					140				
Leu	Ala	Arg	Lys	Ser	Gly	Lys	Phe	Asp	Glu	Glu	Thr	Leu	Gly	Phe	Lys
145					150					155					160
Lys	Arg	Ile	Leu	Gln	Ala	Ser	Gly	Ile	Gly	Asp	Glu	Thr	Tyr	Val	Pro
			165						170					175	
Arg	Ser	Ile	Ser	Ser	Ser	Glu	Asn	Ile	Thr	Thr	Met	Lys	Glu	Gly	Arg
		180					185						190		
Glu	Glu	Ala	Ser	Thr	Val	Ile	Phe	Gly	Ala	Leu	Asp	Glu	Leu	Phe	Glu
	195						200					205			
Lys	Thr	Arg	Val	Lys	Pro	Lys	Asp	Val	Gly	Val	Leu	Val	Val	Asn	Cys
	210					215					220				
Ser	Ile	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Ile	Asn	His
225				230						235					240
Tyr	Lys	Met	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly
				245					250					255	
Cys	Ser	Ala	Gly	Ile	Ile	Ala	Ile	Asp	Leu	Ala	Arg	Asp	Met	Leu	Gln
		260						265					270		
Ser	Asn	Pro	Asn	Ser	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Met	Val	Gly
	275					280						285			
Tyr	Asn	Trp	Tyr	Val	Gly	Ser	Asp	Lys	Ser	Met	Val	Ile	Pro	Asn	Cys
	290					295					300				
Phe	Phe	Arg	Met	Gly	Cys	Ser	Ala	Val	Met	Leu	Ser	Asn	Arg	Arg	Arg
305					310					315					320
Asp	Phe	Arg	His	Ala	Lys	Tyr	Arg	Leu	Glu	His	Ile	Val	Arg	Thr	His
			325						330					335	
Lys	Ala	Ala	Asp	Asp	Arg	Ser	Phe	Arg	Ser	Val	Tyr	Gln	Glu	Glu	Asp
		340						345					350		
Glu	Gln	Gly	Phe	Lys	Gly	Leu	Lys	Ile	Ser	Arg	Asp	Leu	Met	Glu	Val
		355				360						365			
Gly	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val
	370					375					380				
Leu	Pro	Phe	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Ala	Leu	Val	Arg	Arg
385					390					395					400
Thr	Phe	Ser	Pro	Ala	Ala	Lys	Thr	Ser	Thr	Thr	Thr	Ser	Phe	Ser	Thr
			405						410					415	
Ser	Ala	Thr	Ala	Lys	Thr	Asn	Gly	Ile	Lys	Ser	Ser	Ser	Ser	Asp	Leu
		420					425						430		
Ser	Lys	Pro	Tyr	Ile	Pro	Asp	Tyr	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys
	435					440						445			
Phe	His	Ala	Ala	Ser	Lys	Val	Val	Leu	Glu	Glu	Leu	Gln	Lys	Asn	Leu
	450				455						460				
Gly	Leu	Ser	Glu	Glu	Asn	Met	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg
465					470					475					480
Phe	Gly	Asn	Thr	Ser	Ser	Ser	Gly	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Met
		485							490					495	
Glu	Ala	Lys	Glu	Ser	Val	Arg	Arg	Gly	Asp	Arg	Val	Trp	Gln	Ile	Ala
		500						505					510		
Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Val	Val	Trp	Lys	Ala	Met	Arg
	515						520					525			
Lys	Val	Lys	Lys	Pro	Thr	Arg	Asn	Asn	Pro	Trp	Val	Asp	Cys	Ile	Asn
	530					535					540				
Arg	Tyr	Pro	Val	Pro	Leu										
545					550										

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCGAGCTACG	TCAGGGCTTT	TATATGCACA	AATTCTCATA	AAGTTTTCAA	TTTTATTCCA	60
TTTTTCTCGG	AAGCCATGGA	AGCTGCTAAT	GAGCCTGTTA	ATGGCGGATC	CGTACAGATC	120
CGAACAGAGA	ACAACGAAAG	ACGAAAGCTT	CCTAATTTCT	TACAAAGCGT	CAACATGAAA	180
TACGTCAAGC	TAGGTTATCA	TTACCTCATT	ACTCATCTCT	TCAAGCTCTG	TTTGGTTCCA	240
TTAATGGCGG	TTTTAGTCAC	AGAGATCTCT	CGATTAACAA	CAGACGATCT	TTACCAGATT	300
TGGCTTCATC	TCCAATACAA	TCTCGTTGCT	TTCATCTTTC	TCTCTGCTTT	AGCTATCTTT	360
GGCTCCACCG	TTTACATCAT	GAGTCGTCCC	AGATCTGTTT	ATCTCGTTGA	TTACTCTTGT	420
TATCTTCCTC	CGGAGAGTCT	TCAGGTTAAG	TATCAGAAGT	TTATGGATCA	TTCTAAGTTG	480
ATTGAAGATT	TCAATGAGTC	ATCTTTAGAG	TTTCAGAGGA	AGATTCTTGA	ACGTTCTGGT	540
TTAGGAGAAG	AGACTTATCT	CCCTGAAGCT	TTACATTGTA	TCCCTCCGAG	GCCTACGATG	600
ATGGCGGCTC	GTGAGGAATC	TGAGCAGGTA	ATGTTTGGTG	CTCTTGATAA	GCTTTTCGAG	660
AATACCAAGA	TTAACCCTAG	GGATATTGGT	GTGTTGGTTG	TGAATTGTAG	CTTGTTTAAT	720
CCTACACCTT	CGTTGTCAGC	TATGATTGTT	AACAAGTATA	AGCTTAGAGG	GAATGTTAAG	780
AGTTTAAACC	TTGGTGGAAT	GGGGTGTAGT	GCTGGTGTTA	TCTCTATCGA	TTTAGCTAAA	840
GATATGTTGC	AAGTTCATAG	GAATACTTAT	GCTGTTGTGG	TTAGTACTGA	GAACATTACT	900
CAGAATTGGT	ATTTTGGGAA	TAAGAAGGCT	ATGTTGATTC	CGAATTGTTT	GTTTCGTGTT	960
GGTGGTTCGG	CGATTTTGTT	GTCGAACAAG	GGGAAAGATC	GTAGACGGTC	TAAGTATAAG	1020
CTTGTTTATA	CCGTTAGGAC	TCATAAAGGA	GCTGTTGAGA	AGGCTTTCAA	CTGTGTTTAC	1080
CAAGAGCAAG	ATGATAATGG	GAAGACCGGG	GTTTCGTTGT	CGAAAGATCT	TATGGCTATA	1140
GCTGGGGAAG	CTCTTAAGGC	GAATATCACT	ACTTTAGGTC	CTTTGGTTCT	TCCTATAAGT	1200
GAGCAGATTC	TGTTTTTTCAT	GACTTTGGTT	ACGAAGAAAC	TGTTTAACTC	GAAGCTGAAG	1260
CCGTATATTC	CGGATTTCAA	GCTTGCGTTT	GATCATTCTT	GTATCCATGC	TGGTGGTAGA	1320
GCTGTGATTG	ATGAGCTTGA	GAAGAATCTG	CAGCTTTCGC	AGACTCATGT	CGAGGCATCC	1380
AGAATGACAC	TGCACAGATT	TGGAAACACT	TCTTCGAGCT	CGATTGGTGA	TGAATGGGCT	1440
TACATGAGAG	CTAAAGGTAG	GATGAAGAAA	GGAAACCGGG	TTTGGCAGAT	TGCTTTTGGA	1500
AGTGGGTTTA	AGTGTAAACAG	TGCAGTTTGG	GTGGCTCTAA	ACAATGTCAA	GCCTTCGGTT	1560
AGTAGTCCGT	GGGAACACTG	CATCGACCGA	TATCCGGTTA	AGCTCGACTT	C	1611

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser	Ser	Tyr	Val	Arg	Ala	Phe	Ile	Cys	Thr	Asn	Ser	His	Lys	Val	Phe
1				5				10					15		
Asn	Phe	Ile	Pro	Phe	Phe	Ser	Glu	Ala	Met	Glu	Ala	Ala	Asn	Glu	Pro
		20					25					30			
Val	Asn	Gly	Ser	Val	Gln	Ile	Arg	Thr	Glu	Asn	Asn	Glu	Arg	Arg	
	35				40					45					
Lys	Leu	Pro	Asn	Phe	Leu	Gln	Ser	Val	Asn	Met	Lys	Tyr	Val	Lys	Leu
	50				55					60					
Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Leu	Phe	Lys	Leu	Cys	Leu	Val	Pro
65				70						75				80	
Leu	Met	Ala	Val	Leu	Val	Thr	Glu	Ile	Ser	Arg	Leu	Thr	Thr	Asp	Asp
			85						90				95		
Leu	Tyr	Gln	Ile	Trp	Leu	His	Leu	Gln	Tyr	Asn	Leu	Val	Ala	Phe	Ile
		100						105					110		
Phe	Leu	Ser	Ala	Leu	Ala	Ile	Phe	Gly	Ser	Thr	Val	Tyr	Ile	Met	Ser
	115					120					125				
Arg	Pro	Arg	Ser	Val	Tyr	Leu	Val	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro
	130					135					140				
Glu	Ser	Leu	Gln	Val	Lys	Tyr	Gln	Lys	Phe	Met	Asp	His	Ser	Lys	Leu
145				150						155				160	
Ile	Glu	Asp	Phe	Asn	Glu	Ser	Ser	Leu	Glu	Phe	Gln	Arg	Lys	Ile	Leu
			165						170					175	
Glu	Arg	S	r	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	Glu	Ala	Leu
			180						185					190	

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Cys Ile Pro Pro Arg Pro Thr Met Met Ala Ala Arg Glu Glu Ser Glu
 195 200 205
 Gln Val Met Phe Gly Ala Leu Asp Lys Leu Phe Glu Asn Thr Lys Ile
 210 215 220
 Asn Pro Arg Asp Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn
 225 230 235 240
 Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg
 245 250 255
 Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala Gly
 260 265 270
 Val Ile Ser Ile Asp Leu Ala Lys Asp Met Leu Gln Val His Arg Asn
 275 280 285
 Thr Tyr Ala Val Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp Tyr
 290 295 300
 Phe Gly Asn Lys Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg Val
 305 310 315 320
 Gly Gly Ser Ala Ile Leu Leu Ser Asn Lys Gly Lys Asp Arg Arg Arg
 325 330 335
 Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ala Val
 340 345 350
 Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu Gln Asp Asp Asn Gly Lys
 355 360 365
 Thr Gly Val Ser Leu Ser Lys Asp Leu Met Ala Ile Ala Gly Glu Ala
 370 375 380
 Leu Lys Ala Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile Ser
 385 390 395 400
 Glu Gln Ile Leu Phe Phe Met Thr Leu Val Thr Lys Lys Leu Phe Asn
 405 410 415
 Ser Lys Leu Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Asp His
 420 425 430
 Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu Leu Glu Lys
 435 440 445
 Asn Leu Gln Leu Ser Gln Thr His Val Glu Ala Ser Arg Met Thr Leu
 450 455 460
 His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala
 465 470 475 480
 Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Arg Val Trp Gln
 485 490 495
 Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Val Ala
 500 505 510
 Leu Asn Asn Val Lys Pro Ser Val Ser Ser Pro Trp Glu His Cys Ile
 515 520 525
 Asp Arg Tyr Pro Val Lys Leu Asp Phe
 530 535

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCGACGA	TGCCTCAGGC	ACCGATGCCA	GAGTTCCTCTA	GCTCGGTGAA	GCTCAAGTAC	60
GTGAAACTTG	GTTACCAATA	TTTGGTTAAC	CATTTCTTTGA	GTTTCTTTT	GATCCCCGATC	120
ATGGCTATTG	TCGCCGTTGA	GCTTCTTCGG	ATGGGTCCTG	AAGAGATCCT	TAATGTTTGG	180
AATTCACCTC	AGTTTGACCT	AGTTCAGGTT	CTATGTTCTT	CCTTCTTTGT	CATCTTCATC	240
TCCACTGTTT	ACTTCATGTC	CAAGCCACGC	ACCATCTACC	TCGTTGACTA	TTCTTGTTAC	300
AAGCCACCTG	TCACGTGTCG	TGTCCCCTTC	GCAACTTTCA	TGGAACACTC	TCGTTTGATC	360
CTCAAGGACA	AGCCTAAGAG	CGTCGAGTTC	CAAATGAGAA	TCCTTGAACG	TTCTGGCCTC	420
GGTGAGGAGA	CTTGTCTCCC	TCCGGCTATT	CATTATATTC	CTCCACACCC	AACCATGGAC	480
GCGGCTAGAA	GCGAGGCTCA	GATGGTTATC	TTTCGAGGCCA	TGGACGATCT	TTTCAAGAAA	540
ACCGGTCTTA	AACCTAAAGA	CGTCGACATC	CTTATCGTCA	ACTGCTCTCT	TTTCTCTCCC	600

(A) LENGTH: 500 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser 1	Pro	Thr	Met	Pro 5	Gln	Ala	Pro	Met	Pro 10	Glu	Phe	Ser	Ser 15	Val	
Lys	Leu	Lys	Tyr 20	Val	Lys	Leu	Gly	Tyr 25	Gln	Tyr	Leu	Val	Asn 30	His	Phe
Leu	Ser	Phe 35	Leu	Leu	Ile	Pro	Ile 40	Met	Ala	Ile	Val	Ala	Val	Glu	Leu
Leu	Arg 50	Met	Gly	Pro	Glu	Glu 55	Ile	Leu	Asn	Val	Trp 60	Asn	Ser	Leu	Gln
Phe 65	Asp	Leu	Val	Gln 70	Val	Leu	Cys	Ser	Ser	Phe 75	Phe	Val	Ile	Phe	Ile
Ser	Thr	Val	Tyr 85	Phe	Met	Ser	Lys	Pro	Arg 90	Thr	Ile	Tyr	Leu	Val	Asp
Tyr	Ser	Cys 100	Tyr	Lys	Pro	Pro	Val 105	Thr	Cys	Arg	Val	Pro	Phe	Ala	Thr
Phe	Met	Glu 115	His	Ser	Arg	Leu	Ile 120	Leu	Lys	Asp	Lys	Pro	Lys	Ser	Val
Glu 130	Phe	Gln	Met	Arg	Ile	Leu 135	Glu	Arg	Ser	Gly	Leu 140	Gly	Glu	Glu	Thr
Cys 145	Leu	Pro	Pro	Ala 150	Ile	His	Tyr	Ile	Pro	Pro 155	Thr	Pro	Thr	Met	Asp
Ala	Ala	Arg	Ser	Glu 165	Ala	Gln	Met	Val	Ile	Phe 170	Glu	Ala	Met	Asp	Asp
Leu	Phe	Lys 180	Lys	Thr	Gly	Leu	Lys 185	Pro	Lys	Asp	Val	Asp	Ile	Leu	Ile
Val	Asn 195	Cys	Ser	Leu	Phe	Ser	Pro 200	Thr	Pro	Ser	Leu	Ser 205	Ala	Met	Val
Ile 210	Asn	Lys	Tyr	Lys	Leu	Arg 215	Ser	Asn	Ile	Lys	Ser 220	Phe	Asn	Leu	Ser
Gly 225	Met	Gly	Cys	Ser	Ala 230	Gly	Leu	Ile	Ser	Val 235	Asp	Leu	Ala	Arg	Asp
Leu	Leu	Gln	Val	His 245	Pro	Asn	Ser	Asn	Ala 250	Ile	Ile	Val	Ser	Thr	Glu
Ile	Ile	Thr 260	Pro	Asn	Tyr	Tyr	Gln 265	Gly	Asn	Glu	Arg	Ala	Met 270	Leu	Leu
Pro	Asn 275	Cys	Leu	Phe	Arg	Met	Gly 280	Ala	Ala	Ala	Ile	His 285	Met	Ser	Asn
Arg	Arg 290	Ser	Asp	Arg	Trp	Arg 295	Ala	Lys	Tyr	Lys	Leu 300	Ser	His	Leu	Val

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Arg Thr His Arg Gly Ala Asp Asp Lys Ser Phe Tyr Cys Val Tyr Glu
305                               310       315       320
Gln Glu Asp Lys Glu Gly His Val Gly Ile Asn Leu Ser Lys Asp Leu
                               325       330       335
Met Ala Ile Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Ile Gly
                               340       345       350
Pro Leu Val Leu Pro Ala Ser Glu Gln Leu Leu Phe Leu Thr Ser Leu
                               355       360       365
Ile Gly Arg Lys Ile Phe Asn Pro Lys Trp Lys Pro Tyr Ile Pro Asp
                               370       375       380
Phe Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala
385                               390       395       400
Val Ile Asp Glu Leu Gln Lys Asn Leu Gln Leu Ser Gly Glu His Val
                               405       410       415
Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser
                               420       425       430
Ser Leu Trp Tyr Glu Leu Ser Tyr Ile Glu Ser Lys Gly Arg Met Arg
                               435       440       445
Arg Gly Asp Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys
                               450       455       460
Asn Ser Ala Val Trp Lys Cys Asn Arg Thr Ile Lys Thr Pro Lys Asp
465                               470       475       480
Gly Pro Trp Ser Asp Cys Ile Asp Arg Tyr Pro Val Phe Ile Pro Glu
                               485       490       495
Val Val Lys Leu
                               500

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

ATGGACGGTG CCGGAGAATC ACGACTCGGT GGTGATGGTG GTGGTGATGG TTCTGTTGGA      60
GTTCAAGTAT GACAAACACG GATGCTACCG GATTTTCTCC AGAGCGTGAA TCTCAAGTAT      120
GTGAAATTAG GTTACCATTG CTTAATCTCA AATCTCTTGA CTCTCTGTTT ATTCCCTCTC      180
GCCGTTGTTA TCTCCGTCGA AGCCTCTCAG ATGAACCCAG ATGATCTCAA ACAGCTCTGG      240
ATCCATCTAC AATACAATCT GGTAGTATC ATCATCTGTT CAGCGATTCT AGTCTTCGGG      300
TTAACGGTTT ATGTTATGAC CCGACCTAGA CCCGTTTACT TGGTTGATTT CTCTTGTTAT      360
CTCCACCTTG ATCATCTCAA AGCTCCTTAC GCTCGGTTCA TGGAAACATT TAGACTCACC      420
GGAGATTTTC ATGACTCTGC TCTCGAGTTT CAACGCAAGA TCCTTGAGCG TTCTGGTTTA      480
GGGGAAGACA CTTATGTCCC TGAAGCTATG CATTATGTTT CACCGAGAAT TTCAATGGCT      540
GCTGCTAGAG AAGAAGCTGA ACAAGTCATG TTTGGTGCTT TAGATAACCT TTTTCGCTAAC      600
ACTAATGTGA AACCAAAGGA TATTGGAATC CTTGTTGTGA ATTGTAGTCT CTTTAATCCA      660
ACTCCTTCGT TATCTGCAAT GATTGTGAAC AAGTATAAGC TTAGAGGTAA CATTAGAAGC      720
TACAATCTAG GCGGTATGGG TTGCAGCGCG GGAGTTATCG CTGTGGATCT TGCTAAAGAC      780
ATGTTGTTGG TACATAGGAA CACTTATGCG GTTGTGTTT CTACTGAGAA CATTACTCAG      840
AATTGGTATT TTGGTAACAA GAAATCGATG TTGATACCGA ACTGCTTGTT TCGAGTTGGT      900
GGCTCTGCGG TTTTGCTATC GAACAAGTCG AGGGACAAGA GACGGTCTAA GTACAGGCTT      960
GTACATGTAG TCAGGACTCA CCGTGGAGCA GATGATAAAG CTTTCCGTTG TGTATTATCA      1020
GAGCAGGATG ATACAGGGAG AACCGGGTTT TCGTTGTCGA AAGATCTAAT GGCGATTGCA      1080
GGGGAAATCT TCAAAACCAA TATCACTACA TTGGGTCTCT TTGTTCTACC GATAAGTGAG      1140
CAGATTCTCT TCTTTATGAC TCTAGTTGTG AAGAAGCTCT TTAACGGTAA AGTGAAACCG      1200
TATATCCCGG ATTTCAAAC TGTCTTCGAG CATTTCTGTA TCCATGCTGG TGGAAGAGCT      1260
GTGATCGATG AGTTAGAGAA GAATCTGCAG CTTTCACCAG TTCATGTCGA GGCTTCGAGG      1320
ATGACTCTTC ATCGATTTGG TAACACATCT TCGAGCTCCA TTTGGTATGA ATTGGCTTAC      1380
ATTGAAGCGA AGGGAAGGAT GCGAAGAGGT AATCGTGTGT GGCAAATCGC GTTCGGGAAGT      1440
GGATTTAAAT GTAATAGCGC GATTTGGGAA GCATTAAGGC ATGTGAAACC TTCGAACAAC      1500
AGTCCTTGGG AAGATTGTAT TGACAAGTAT CCGGTAACCT TAAGTTAT      1548

```

(2) INFORMATION FOR SEQ ID NO:14:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Asp Gly Ala Gly Glu Ser Arg Leu Gly Gly Asp Gly Gly Gly Asp
 1      5      10      15
Gly Ser Val Gly Val Gln Ile Arg Gln Thr Arg Met Leu Pro Asp Phe
 20      25      30
Leu Gln Ser Val Asn Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu
 35      40      45
Ile Ser Asn Leu Leu Thr Leu Cys Leu Phe Pro Leu Ala Val Val Ile
 50      55      60
Ser Val Glu Ala Ser Gln Met Asn Pro Asp Asp Leu Lys Gln Leu Trp
 65      70      75      80
Ile His Leu Gln Tyr Asn Leu Val Ser Ile Ile Ile Cys Ser Ala Ile
 85      90      95
Leu Val Phe Gly Leu Thr Val Tyr Val Met Thr Arg Pro Arg Pro Val
 100     105     110
Tyr Leu Val Asp Phe Ser Cys Tyr Leu Pro Pro Asp His Leu Lys Ala
 115     120     125
Pro Tyr Ala Arg Phe Met Glu His Ser Arg Leu Thr Gly Asp Phe Asp
 130     135     140
Asp Ser Ala Leu Glu Phe Gln Arg Lys Ile Leu Glu Arg Ser Gly Leu
 145     150     155     160
Gly Glu Asp Thr Tyr Val Pro Glu Ala Met His Tyr Val Pro Pro Arg
 165     170     175
Ile Ser Met Ala Ala Ala Arg Glu Glu Ala Glu Gln Val Met Phe Gly
 180     185     190
Ala Leu Asp Asn Leu Phe Ala Asn Thr Asn Val Lys Pro Lys Asp Ile
 195     200     205
Gly Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu
 210     215     220
Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly Asn Ile Arg Ser
 225     230     235     240
Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ala Val Asp
 245     250     255
Leu Ala Lys Asp Met Leu Leu Val His Arg Asn Thr Tyr Ala Val Val
 260     265     270
Val Ser Thr Glu Asn Ile Thr Gln Asn Trp Tyr Phe Gly Asn Lys Lys
 275     280     285
Ser Met Leu Ile Pro Asn Cys Leu Phe Arg Val Gly Gly Ser Ala Val
 290     295     300
Leu Leu Ser Asn Lys Ser Arg Asp Lys Arg Arg Ser Lys Tyr Arg Leu
 305     310     315     320
Val His Val Val Arg Thr His Arg Gly Ala Asp Asp Lys Ala Phe Arg
 325     330     335
Cys Val Tyr Gln Glu Gln Asp Asp Thr Gly Arg Thr Gly Val Ser Leu
 340     345     350
Ser Lys Asp Leu Met Ala Ile Ala Gly Glu Thr Leu Lys Thr Asn Ile
 355     360     365
Thr Thr Leu Gly Pro Leu Val Leu Pro Ile Ser Glu Gln Ile Leu Phe
 370     375     380
Phe Met Thr Leu Val Val Lys Lys Leu Phe Asn Gly Lys Val Lys Pro
 385     390     395     400
Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys Ile His Ala
 405     410     415
Gly Gly Arg Ala Val Ile Asp Glu Leu Glu Lys Asn Leu Gln Leu Ser
 420     425     430
Pro Val His Val Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn
 435     440     445

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[illegible]

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WHAT IS CLAIMED IS:

1. An isolated polynucleotide encoding a polypeptide having an amino acid sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an amino acid sequence substantially identical to SEQ ID NO:14.
2. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:2.
3. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:4.
4. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:6.
5. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:8.
6. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:10.
7. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:12.
8. The polynucleotide of claim 1, wherein said amino acid sequence is SEQ ID NO:14.

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9. An isolated polynucleotide, wherein said polynucleotide is selected from the group consisting of:

- a) SEQ ID NO:1;
- b) SEQ ID NO:3;
- c) SEQ ID NO:5;
- d) SEQ ID NO:7;
- e) SEQ ID NO:9;
- f) SEQ ID NO:11;
- g) SEQ ID NO:13;
- h) an RNA analog of SEQ ID NO:1;
- i) an RNA analog of SEQ ID NO:3;
- j) an RNA analog of SEQ ID NO:5;
- k) an RNA analog of SEQ ID NO:7;
- l) an RNA analog of SEQ ID NO:9;
- m) an RNA analog of SEQ ID NO:11;
- n) an RNA analog of SEQ ID NO:13;
- o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
- p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

10. An isolated polypeptide having an amino acid sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an

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amino acid sequence substantially identical to SEQ ID NO:14.

11. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:2.

12. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:4.

13. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:6.

14. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:8.

15. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:10.

16. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:12.

17. The polypeptide of claim 10, wherein said amino acid sequence is SEQ ID NO:14.

18. A transgenic plant containing a nucleic acid construct comprising a polynucleotide selected from the group consisting of:

- a) SEQ ID NO:1;
- b) SEQ ID NO:3;
- c) SEQ ID NO:5;
- d) SEQ ID NO:7;
- e) SEQ ID NO:9;
- f) SEQ ID NO:11;
- g) SEQ ID NO:13;
- h) an RNA analog of SEQ ID NO:1;

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- i) an RNA analog of SEQ ID NO:3;
- j) an RNA analog of SEQ ID NO:5;
- k) an RNA analog of SEQ ID NO:7;
- l) an RNA analog of SEQ ID NO:9;
- m) an RNA analog of SEQ ID NO:11;
- n) an RNA analog of SEQ ID NO:13;
- o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
- p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14.

19. The plant of claim 18, wherein said construct further comprises a regulatory element operably linked to said polynucleotide.

20. The plant of claim 19, wherein said regulatory element is a tissue-specific promoter.

21. The plant of claim 20, wherein said regulatory element is an epidermal cell-specific promoter.

22. The plant of claim 20, wherein said regulatory element is a seed-specific promoter that is operably linked in sense orientation to said polynucleotide.

23. The plant of claim 22, wherein said plant has altered levels of very long chain fatty acids in seeds compared to the levels in a plant lacking said nucleic acid construct.

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24. A transgenic plant containing a nucleic acid construct comprising a polynucleotide encoding a polypeptide selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:2, an amino acid sequence substantially identical to SEQ ID NO:4, an amino acid sequence substantially identical to SEQ ID NO:6, an amino acid sequence substantially identical to SEQ ID NO:8, an amino acid sequence substantially identical to SEQ ID NO:10, an amino acid sequence substantially identical to SEQ ID NO:12, and an amino acid sequence substantially identical to SEQ ID NO:14.

25. The plant of claim 24, wherein said construct further comprises a regulatory element operably linked to said polynucleotide.

26. The plant of claim 25, wherein said regulatory element is a tissue-specific promoter.

27. The plant of claim 26, wherein said regulatory element is an epidermal cell-specific promoter.

28. The plant of claim 26, wherein said regulatory element is a seed-specific promoter that is operably linked in sense orientation to said polynucleotide.

29. The plant of claim 28, wherein said plant has altered levels of very long chain fatty acids in seeds compared to the levels in a plant lacking said nucleic acid construct.

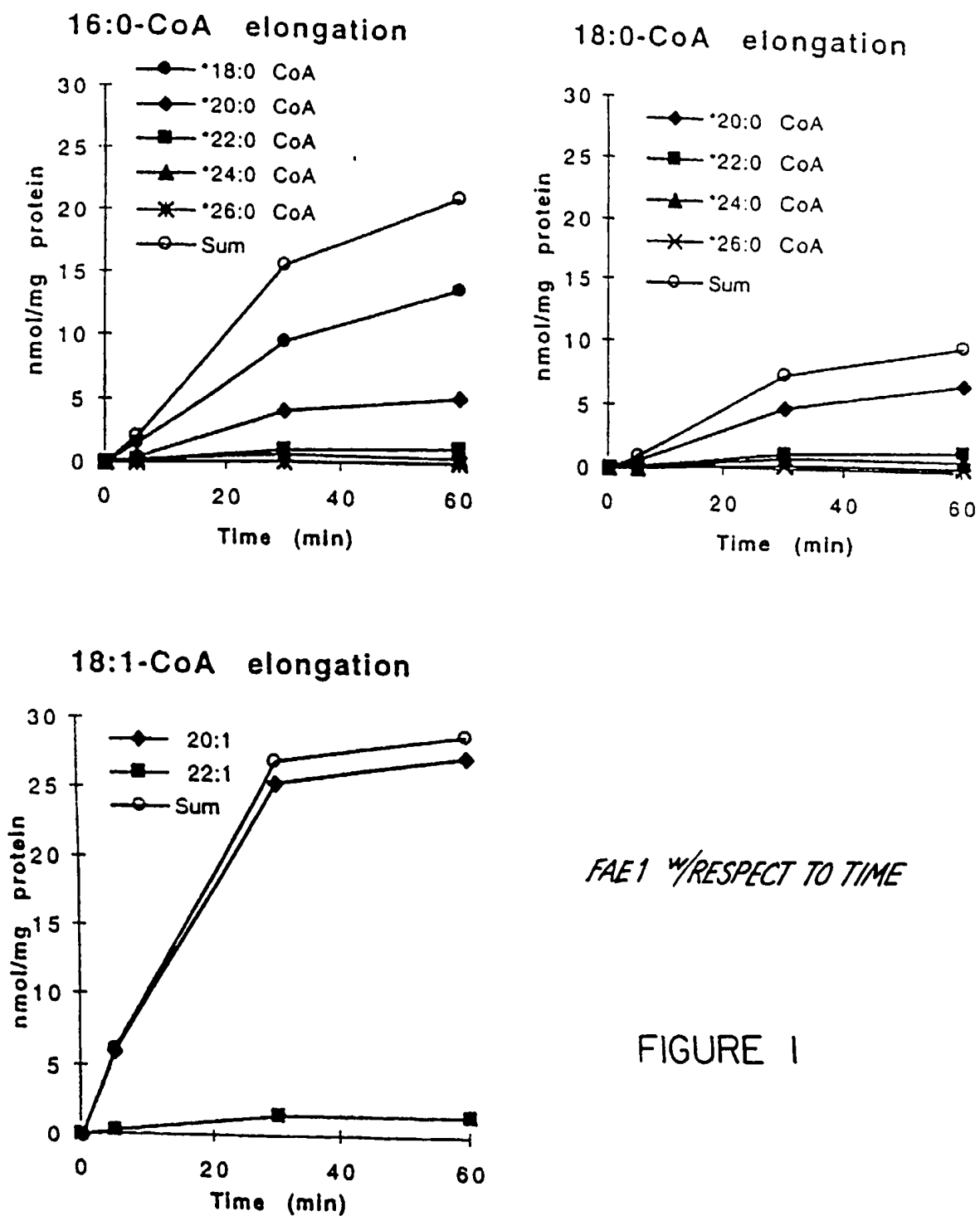
30. A method of altering the levels of very long chain fatty acids in a plant, comprising the steps of:

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A) creating a nucleic acid construct, said construct comprising a polynucleotide selected from the group consisting of:

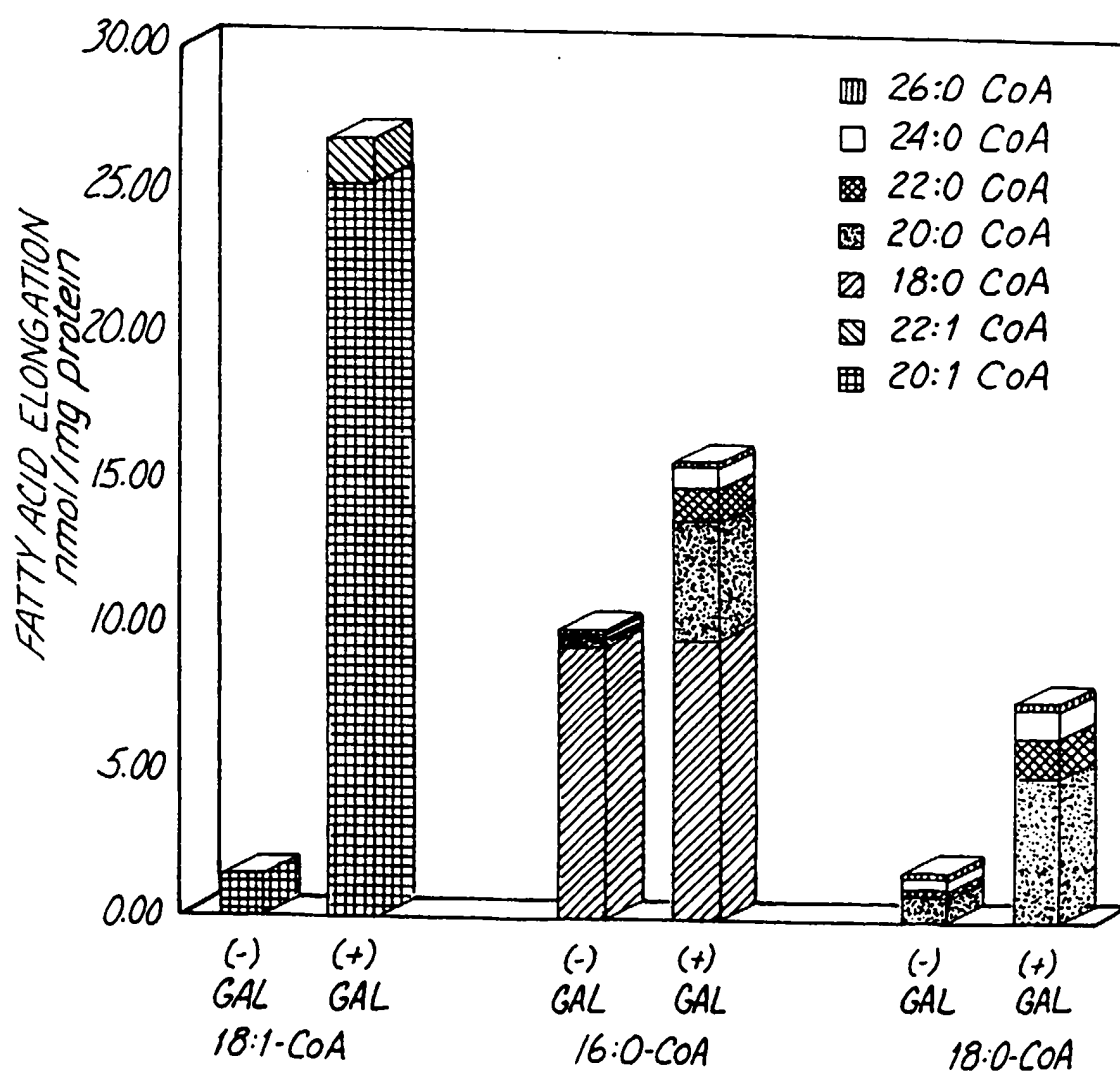
- a) SEQ ID NO:1;
 - b) SEQ ID NO:3;
 - c) SEQ ID NO:5;
 - d) SEQ ID NO:7;
 - e) SEQ ID NO:9;
 - f) SEQ ID NO:11;
 - g) SEQ ID NO:13;
 - h) an RNA analog of SEQ ID NO:1;
 - i) an RNA analog of SEQ ID NO:3;
 - j) an RNA analog of SEQ ID NO:5;
 - k) an RNA analog of SEQ ID NO:7;
 - l) an RNA analog of SEQ ID NO:9;
 - m) an RNA analog of SEQ ID NO:11;
 - n) an RNA analog of SEQ ID NO:13;
 - o) a polynucleotide having a nucleic acid sequence complementary to a), b), c), d), e), f), g), h), i), j), k), l), m), or n); and
 - p) a nucleic acid fragment of a), b), c), d), e), f), g), h), i), j), k), l), m), n), or o) that is at least 15 nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, or SEQ ID NO:14; and
- B) introducing said construct into said plant, wherein said polynucleotide is effective for altering the levels of very long chain fatty acids in said plant.

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FIGURE 2



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EL1 1560 bases
 ATGGATCGAG AGAGATTAAAC GGCGGAGATG GCGTTTCGAG ATTCAATCATC GGCCGTTATA
 AGAATTTCGAA GACGTTTGCC GGATTTATTA ACGTCCGTTA AGCTCAAATA CGTGAAGCTT
 GGACTTCACA ACTCTTGCAA GGTGTTTCA GCTAACCGGT CTACGTTTCG ATACGTTCTC TTTCCCTCTCC
 ACCGGAACCG TGCTGGTTCA CGGTTCAACT CGACACGGCG TCTAACCCGG TTTACCTAGT GGATTTCTCC
 TCTAACACAGG CCTCTACGT CGGAAGACGA GCGTAAATA TCAGTAGATT CGTTCTTGAC GATGACTGAG
 TTCGTTTGA CCTCTACGT GGCTAACCCG GCTAACCCGG TCTAACCTAGT TTTACCTAGT GGATTTCTCC
 TGCTACAAAC CGGAAGACGA GCGTAAATA TCAGTAGATT CGTTCTTGAC GATGACTGAG
 GAAAATGGAT CATTACCGA TGACACGGTT CAGTTCCAGC AAAGAAATCTC GAACCGGGCC
 GGTTTGGGAG ACGAGACGTA TCTGCCACGT TCTGCCACGT GGCAATAACTT CAACGCCCCC GAAGCTAAAT
 ATGTCAGAGG CACGTGCCGA AGCTGAAGCC GGTATGTTTG GAGCCTTAGA TTCCCTCTTC
 GAGAAAACCG GAATTAACC GGCCGAAGTC GGAATCTTGA TAGTAAACTG CAGCTTATTC
 AATCCGACGC CGTCTCTATC AGCGATGATC GTGAACCATT ACAAGATGAG AGAAGACATC
 AAAAGTTACA ACCTCGGAGG AATGGGTTGC TCCGCCGGAT TAATCTCAAT CGATCTCGCT
 AACAACTCTC TCAAAGCAAA CCTAATCTT TACGCTGTCC TGGTAAGCAC GGAAACATA
 ACCCTAAACT GGACTTCGG AAATGACCGG TCAATGCTCC TCTGCAACTG CATCTTCCGA
 ATGGGCGGAG CTGCGATTCT CCTCTCTAAC CGCCGTCAAG ACCGGAAGAA GTCAAAGTAC
 TCGCTGGTCA ACGTCGTTCC AACACATAAA GGATCAGACG ACAAGAACTA CAATTGCCGTG
 TACCAGAAAG AAGACGAGAG AGGAACAATC GGTGTCTCTT TAGCTAGAGA GCTCATGTCT
 GTCGCCGGAG ACGCTCTGAA AACAAACATC ACGACTTTAG GACCGATGGT TCTTCCATTG
 TCAGAGCAGT TGATGTTCTT GATTTCCTTG GTCAAAAAGGA AGATGTTCAA GTTAAAGATT
 AAACCGTATA TTCCGGATTT CAAGCTAGCT TTCGAGCATT TCTGTATTCA CGCAGGAGGT
 AGAGCGGTTT TAGACGAAGT GCAGAAAGAT CTTGATCTCA AAGATTGGCA CATGGAACCT
 TCTAGAATGA CTTTGACACAG ATTTGGTAAC ACTTCGAGTA GCTCGCTTTG GTATGAGATG
 GCTTATACCG AAGCTAAGG TCGGGTTAAA GCTGGTGACC GACTTTGGCA GATTGCGTTT
 GGATCGGGT TCAAGTGTA TAGTGCGGTT TGGAAAGCGT TACGACCGGT TTCGACGGAG
 GAGATGACCG GTAATGCTTG GGCTGGTTCC ATTGATCAAT ATCCCGTTAA AGTTGTGCAA

EL1

FIGURE 3

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EL1 sequence
 Molecular Weight 58379.00 Daltons
 520 Amino Acids
 62 Strongly Basic(+) Amino Acids (K,R)
 52 Strongly Acidic(-) Amino Acids (D,E)
 187 Hydrophobic Amino Acids (A,I,L,F,W,V)
 144 Polar Amino Acids (N,C,Q,S,T,Y)
 8.784 Isoelectric Point
 10.804 Charge at PH 7.0

MDRERLTAEM	AFRDSSSAVI	RIRRRLPDLL	TSVKLKYYVKL	GLHNSCNVTT	ILFFLIILPL
TGTVLVQLTG	LTFDTFSELW	SNQAVQLDTA	TRLTCLVFLS	FVLTLYVANR	SKPVYLVDFS
CYKPEDERKI	SVDSFLTMTTE	ENGSTDDTV	QFQQRISNRA	GLGDETYLPR	GITSTPPKLN
MSEARAEAEA	VMFGALDSLF	EKTGIKPAEV	GILIVNCSLF	NPTPSLSAMI	VNHYKMREDI
KSYNLGGMGC	SAGLISIDLA	NNLLKANPNS	YAVVVSTENI	TLNWFYGNDR	SMLLCNCIFR
MGGAAILLNS	RRQDRKKSKY	SLVNVVRTHK	GSDDKNYNVCV	YQKEDERGTI	GVSLARELMS
VAGDALKTNI	TTLGPMVLPL	SEQLMFLISL	VKRKMFKLV	KPYIPDFKLA	FEHFCIHAGG
RAVLDEVQKN	LDLKDWHMEP	SRMTLHRFCN	TSSSSLWYEM	AYTEAKGRVK	AGDRLWQIAF
GSGFKCNSAV	WKALRPVSTE	EMTGNAWAGS	IDQYPVKVVQ		

FIGURE 4

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EL2 1479 bases
 ATGGATTACC CCATGAAGAA GGTAATAATC TTTTCAACT ACCTCATGGC GCATCGCTTC 120
 AAGCTCTGCT TCTTACCATT AATGGTTGCT ATAGCCGTGG AGGCGTCTCG TCTTTCCACA
 CAAGATCTCC AAAACTTTTA CCTCTACTTA GTCGACTCTT TACCTCATGA CCCGGCCCAA ACCCGTTTAT 240
 TTCCTTTACC TCGCTCTCGG CCTCCACCCG CTGCACTCA AGCCAGCAC CCAGAGGATC
 CTCGTTGACT TTAGCTGCTA ACGAGAAGCA GCGCGTGA GCAAGAGTC CGATTACTTG 360
 ATGCAACACG TAAGGCTTGT TCTAGAAAGT TCCGGTCTAG GCCAAGAGAC GTACGTACCC
 ATGGACTTCT GCGAGAAGAT ACTACAACAG AATTGGCTG TATCACGTAT AGAGACGGAG 480
 GAAGGCTTTC AAACTTTGCC CGATAATCTG TTTTCGCAACA CGGAATAAG CCTAGTGAT
 GAAGTTATTA TTGGTGCGGT TTCAAGCACT TTAAATCCAA CACCTTCGCT ATCAAGTATC 600
 ATAGGTATAT TGGTGGTGAA TAGGGATAAT ATAAAGAGCT TGAATCTTGG TGGGATGGGG
 TTAGTGAATA AGTTTAAACT TATCGATGCG GCTAAGAGCT TGTACAAGT TCATAGAAAC 720
 TGTAGCGCTG GAGTCATCGC CACGGAGAAC ATCACTCAA ACTTGTACAT GGTAAACAAC
 ACTTATGCTC TTGTGGTGAG CTGTTTGTTT CGTATAGGTG GGGCCGCGAT TTTGCTTTCT 840
 AAATCAATGT TGGTTACAAA ACGCGCAAAA TACGAGCTTG TTCACACCGT GCGGGTCCAT
 AACCGGTCTA TAGATCGTAA CTATGAATGT GCAACTCAAG AAGAGGATGA AGATGGCATA 960
 ACCGGAGCAG ATGACCGATC GAATCTACCA ATGGTAGCTG CAAGAACCCT AAAGATCAAT
 GTTGGGGTTT CCTTGTCAA TGTCTTCCC ATAGCGGAGA AGTTTCACTT CTTTGTGAGG 1080
 ATCGCAACTT TGGTCCGCT CAACCCCAA GGTAGAGCGC TAATTGATGA GATGGAGAAG 1200
 TTCGTTAAAA AGAAGTTTCT CCATGCGGGT GCTTCAAGAA TGACATTACA CAGGTTTGGT
 GCATTCGAGC ATTTCTGTAT AGACGTTGAG TTGGCTTACA CAGAAGCCAA AGGAAGGATG 1320
 AATCTTCATC TAACCTCCAT TTGGTACGAG TTGGGGTCAG GTTTTAAGTG TAATAGTTCA
 AATACCTCTT CGAGCTCCAT GCAGATTGCG TCTACTAATA ATCCTTGGGA ACAGTGTCTA 1440
 ACGAAAGGAG ATAGGATTG CGTCAAGCCT CGATATAGAT TTAAAAGAG

EL2
FIGURE 5

EL2 protein sequence

Molecular Weight 55799.30 Daltons

493 Amino Acids

55 Strongly Basic(+) Amino Acids (K,R)

46 Strongly Acidic(-) Amino Acids (D,E)

181 Hydrophobic Amino Acids (A,I,L,F,W,V)

134 Polar Amino Acids (N,C,Q,S,T,Y)

8.756 Isoelectric Point

10.995 Charge at PH 7.0

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MDYPMKKVKI FFNYLMAHRF KLCFLPLMVA IAVEASRLST QDLQNFYLYL QNNHTSLTMF FLYLALGSTL
 YLMTRPKPVY LVDFSCYLPP SHLKASTQRI MQHVRLLVREA GAWKQESDYL MDFCEKILER SGLGQETYVP
 EGLQTLPLQQ NLAVSRLETE EVIIGAVDNL FRNTGISPSD IGILVVNSST FNPTPSLSSI LVNKFKLARDN
 IKSLLNLGGMG CSAGVIAIDA AKSLLQVHRN TYALVVSTEN ITQNLVGMNN KSMVLVTNCLF RIGGAAILLS
 NRSIDRKRAK YELVHTVRVH TGADDRSYEC ATQEEDEDDGI VGVSLSKNLP MVAARTLKIN IATLGPLVLP
 ISEKFHFFVR FVKKKFLNPK LKHYIIPDFKL AFEHFCIHAG GRALIDEMEK NLHLTPLDVE ASRMTLHRFG
 NTSSSSIWEY LAYTEAKGRM TKGDRIWQIA LGSGFKCNSS VWVALRNVKP STNNPWEQCL HKYYPVEIDID
 LKE

FIGURE 6

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EL3 1512 bases

CTACGTCAGG GTAGAACA AAA GAGTAAACAC TTAAGCAAAA CAATTGTGCC TACTCTTAGG TTATCTCCAA
TGAAGAACTT AAAGATGGTT TTCTTCAAGA TCCTCTTTAT CTCCTTAATG GCAGGATTAG CCATGAAAGG
ATCTAAGATC AACGTAGAAG ATCTCCAAA ATCTCCCTC GTTCCTCTCT TGGATCCTCT ACATGTTAAC CCGACCTAAA CCCGTTTACC
AGCCTTCTAT TGTTCCTTGT CGTTTTCCTG CTTCACCCGT CCGATCTCAA GGTCAGTATC CAAACCCCTAA TGGGACACGC
TTGTTGATTT CTCCTGCTAC GCATGTGTTG GAAGAACA AAA GAGAGCGACC ATTTAGTTGA CTTCCAGGAG
AAGACGTGCA AGAGAAGCAG AACGTTCCGG TCTTGGTCAA GAAACCTACA TCCCCGAGGG TCTTCAGTGC TTCCCACTTC
AAGATTCTTG AACGTTCCGG ATGATATCGG TATATTGGTG GTGAATTCTA GCACGTTTAA TCCAACCTCCA
AGCAAGGCAT GGGTGCTTCA CGTAAAGAGA CGGAAGAAGT AATCTTCGGA GAGTTTGAAT CTTGGAGGGA
CAACACCCGG GTAAAACCTG CCAATGATTGT GAACAAGTAC AACTCAGAG AACAACATCAA GAGTTTGAAT CTTGGAGGGA
TCACTCGCCT TGCCGGAGTT ATAGCTGTTG ATGTCGCTAA GGGATTACTA CAAAGTTTCA GGAACACTTA
TGGGTTGCAG GTAAAGCAG ATAAGCAGTAC AGAACAATCAC TCAGAACTTA TACTTGGGGA AAAACAATC AATGCTAGTC
TGCTATTGTA GTAAAGCAG ATAAGCAGTAC AGAACAATCAC TCAGAACTTA TACTTGGGGA AAAACAATC AATGCTAGTC
ACAAACTGTT TGTTCGCGT TGGTGGTGTG TGGTGGTGTG TGGTGGTGTG TGGTGGTGTG TGGTGGTGTG TGGTGGTGTG
CCAAATACGA GCTTGTTCAC ACCGTACCGA TCCATACCGG ATCAGATGAT AGGTCGTTTCG AATGTGCGAC
ACAAAGAGAG GATGAAGATG GTATAATTGG AGTTACCTTG ACAAAGAATC TACCTATGTT GGCTGCAAGG
ACTCTTAAGA TAAATATCGC AACTTTGGGT CCTCTTGTTAC TTCCATTAAA AGAGAAGCTA GCCTTCTTTA
TTACTTTTGT CAAGAAGAAG TATTTCAGC CAGAGTTAAG GAATTATACA CCAGATTTC AAGCTTGCCCTT
TGAGCATTTT TGTATCCACG CTGGTGGGAG AGCTCTAATA GATGAGCTGG AGAAGAACCT TAAGCTTTCT
CCGTTACACG TAGAGGCGTC AAGAATGACA CTACACAGGT TTGGTAACAC TTCTTCTAGC TCAATCTGGT
ACGAGTTAGC TTATACAGAA GCTAAAGGAA GGATGAAGGA AGGAGATAGG ATTTGGCAGA TTGCTTTGGG
GTCAGGTTT AAGTGTAACA GTTCAGTATG GGTGGCTCTG CGAGACGTTA AGCCTTCAGC TAACAGTCCA
TGGGAAGACT GTATGGATAG ATATCCGGTT GAGATTGATA TT

EL3

FIGURE 7

EL3 protein sequence
Molecular Weight 56801.10 Daltons
504 Amino Acids
66 Strongly Basic(+) Amino Acids (K,R)
48 Strongly Acidic(-) Amino Acids (D,E)
183 Hydrophobic Amino Acids (A,I,L,F,W,V)
127 Polar Amino Acids (N,C,Q,S,T,Y)
9.315 Isoelectric Point
19.797 Charge at PH 7.0

LRQGRTKSKH LSKTICPTLR LSPMKNLKMW FFKILFISLM AGLAMKGSKI NVEDLQKFSL HHTQNNLQTI
SLLFLVVFV WILYMLTRPK PVYLVDVFCY LPPSHLKVSI QTLMGHARRA REAGMCWKNK ESDHLVDFQE
KILERSGLGQ ETYIPEGLQC FPLQQGMGAS RKETEEVIFG IAVDVAKGLL QVHRNTYAIV VSTENITQNL YLGKNKSMVLV
SLASMIVNKY KLRDNIKSLN LGMGCSAGV TVRIHTGSDD RSFECATQEE DEDGIIGVTL TKNLPMVAAR
TNCLFRVGGG AVLLSNRSD RNRKAYELVH AFFITFVKKK YFKPELRNYT PDFKLAFEHF CIHAGGRALI DELEKNLKLS
TLKINIATLG PLVPLKEKL SIWYELAYTE AKGRMKEGDR IWQIALGSGF KCNSSVWVAL RDVKPSANSP
PLHVEASRMT LHRFGNTSSS WEDCMDRYPV EIDI

EL3
FIGURE 8

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EL4 cDNA 1650 bases

ATGGGTAGAT CCAACGAGCA AGATCTGCTC TCTACCGAGA TCGTTAATCG TGGGATCGAA CCATCCGGTC
CTAACGCCGG CTCACCAACG TTCTCGGTTA GGTTCAGGAG ACGTTTGCCCT GATTTCTTIC AGTCGGTGAA
CTTGAAGTAC GTGAAACTTG GTTACCACTA CCTCATAAAC CATGCGGTTT ATTTGGCGAC CATACCGGTT
CTTGTGCTGG TTTTTAGTGC TGAGGTTGGG AGTTTAAGCA AGTTTAAAGAT TTGGAAGAAG CTTTGGGACT
ATGATCTTGC AACTGTTATC GGATTCCTCG GTGTCCTTGT TTTAACCGCT TGTGCTTACT TCATGTCTCG
TCCTCGCTCT GTTTATCTTA TTGATTTGCG TTGTTACAAG CCTCCGATG AACACAAGGT GACAAAAGAA
GAGTTCATAG AACTAGCGAG AAATCAGGG AAGTTCGACG AAGAGACACT AAGAGGATCT AAGAGGATCT
TACAAGCCTC AGGCATAGGC GACGAGACAT ACGTCCCAAG ATCCATCTCT TCATCAGAAA ACATAACAAC
GATGAAAGAA GTCGTGAAG AAGCCTCTAC AGTGATCTTT GGAGCACTAG ACGAACTCTT CGAGAAGACA
CGTGTAAGAA CTAAAGACGT TGGTGTCCTT GTGGTTAACT GTAGCATTTT CAACCCGACA CCGTCGTGT
CCGCAATGGT GATAAACCAT TACAAGATGA GAGGGAACAT ACTTAGTTAC AACCTTGGAG GGATGGGATG
TTCGGCTGGA ATCATAGCTA TTGATCTTGC TCGTGACATG CTTCAGTCTA ACCCTAATAG TTATGCTGTT
GTTGTGAGTA CTGAGATGGT TGGGTATAAT TGGTACGTGG GAAAGTGACAA GTCAATGGTT ATACCTAATT
GTTTCTTTAG GATGGGTTGT TCTGCCGTTA TGCTCTCTAA CCGTCGTCGT GACTTTCGCC ATGCTAAGTA
CCGTCTCGAG CACATTGTCC GAACCTCATAA GGCTGCTGAC GACCGTAGCT TCAGGAGTGT GTACCAAGAA
GAAGATGAAC AAGGATTCAA GGGGTTGAAG ATAAGTAGAG ACTTAATGGA AGTTGGAGGT GAAAGCTCTCA
AGACAAACAT CACTACCTTA GGTCCTCTTG TCCTACCTTT CTCCGAGCAG CTTCTCTTCT TTGCTGCTTT
GGTCCGCCGA ACATTCTCAC CTGCTGCCAA AACGTCCACA ACCACTTCTT TCTCTACTTC CGCCACCGCA
AAAACCAATG GAATCAAGTC TTCCCTCTCC GATCTGTCCA AGCCATACAT CCCGGACTAC AAGCTCGCCT
TCGAGCATTT TTGCTTCCAC GCGGCAAGCA AAGTAGTGCT TGAAGAGCTT CAAAAGAATC TAGGCTTGAG
TGAAGAGAAAT ATGGAGGCTT CTAGGATGAC ACTTCACAGG TTTGGAAACA CTTCTAGCAG TGGATCTGG
TATGAGTTGG CTTACATGGA GGCCAAGGAA AGTGTTCTGTA GAGGCGATAG GGTTTGGCAG ATCGCTTTCG
GTTCTGGTTT TAAGTGTAAC AGTGTTGGTGT GGAAGGCAAT GAGGAAGGTG AAGAAGCCAA CCAGGAACAA
TCCTTGGGTG GATTGCATCA ACCGTTACCC TGTGCCCTCTC

EL4
FIGURE 9

EL4 protein sequence
Molecular Weight 61953.80 Daltons
550 Amino Acids
71 Strongly Basic(+) Amino Acids (K,R)
58 Strongly Acidic(-) Amino Acids (D,E)
191 Hydrophobic Amino Acids (A,I,L,F,W,V)
147 Polar Amino Acids (N,C,Q,S,T,Y)
9.036 Isoelectric Point
14.349 Charge at PH 7.0

MGRSNEQDLL STEIVNRGIE PSGPNAGSPT FSVRVRRRLP DFLQSVNLKY VKLGYHYLIN HAVYLATIPV
LVLVFSAEVG SLSREEIWKK LWDYDLATVI GFFGVFVLTA CVYFMSRPRS VYLIDFACYK PSDEHKVTKE
EFIELARKSG KFDEETLGFK KRILQASGIG DETYVPRSIS SSENITTMKE GREESTVIF GALDELFEKT
RVKPKDVGV L VVNC SIFNPT PSLSAMVINH YKMRGNILSY NLGGMGCSAG IIAIDLARDM LQSNPNSYAV
VVSTEMVGYN WYVGSDKSMV IPNCFRFGC SAVMLSNRRR DFRHAKYRLE HIVRTHKAD DRSFRSVYQE
EDEQGFKGLK ISRDLMEVGG EALKTNITTL GPLVLPFSEQ LLFFAALVRR TFSPAAKTST TTSFSTSATA
KTNIGIKSSSS DLSKPYIPDY KLAFEHFHCFH AASKVVLEEL QKNLGLSEEN MEASRMTLHR FGNTSSSGIW
YELAYMEAKE SVRRGDRVWQ IAFSGGFKCN SVVWKAMRKV KKPTRNNPWV DCINRYPVPL

EL4
FIGURE 10

EL5 cDNA 1611 bases

TCGAGCTACG TCAGGGCTTT TATATGCACA AATCTCATA AAGTTTTCAA TTTTATTCCA TTTTCTCGG
AAGCCATGGA AGCTGCTAAT GAGCCTGTTA ATGGCGGATC CGTACAGATC CGAACAGAGA ACAACGAAAG
ACGAAAGCTT CCTAATTCTT TACAAGCGT CAACATGAAA TACGTCAAGC TAGGTTATCA TTACCTCAT
ACTCATCTCT TCAAGCTCTG TTTGGTTCCA TTAATGGCGG TTTTAGTCAC AGAGATCTCT CGATTACAA
CAGACGATCT TTACCAGATT TGGCTTCATC TCCAATACAA TCTCGTTGCT TTCATCTTTC TCTCTGCTTT
AGCTATCTTT GGCTCCACCG TTTACATCAT GAGTCGTCCC AGATCTGTTT ATCTCGTTGA TTACTCTTGT
TATCTTCCTC CGGAGAGTCT TCAGGTTAAG TATCAGAAAT TATGGATCA TTCTAAGTTG ATTGAAGATT
TCAATGAGTC ATCTTTAGAG TTTCAGAGGA AGATTCTTGA ACGTTCTGGT TTAGGAGAAAG AGACTTATCT
CCCTGAAGCT TTACATTGTA TCCCTCCGAG GCCTACGATG ATGGCGGCTC GTGAGGAATC TGAGCAGGTA
ATGTTTGGTG CTCTTGATAA GCTTTTCGAG AATACCAAGA TTAACCCCTAG GGATATTGGT GTGTTGGTTG
TGAATTGTAG CTTGTTTAAAT CCTACACCTT CGTTGTCAGC TATGATTGTT AACAAGTATA AGCTTAGAGG
GAATGTTAAG AGTTTAAACC TTGGTGGAAT GGGGTGTAGT GCTGGTGTTA TCTCTATCGA TTTAGCTAAA
GATATGTTGC AAGTTCATAG GAATACTTAT GCTGTTGTGG TTAGTACTGA GAACATTACT CAGAATTGGT
ATTTTGGGAA TAAGAAAGCT ATGTTGATTC CGAATTGTTT GTTTCGTGTT GGTGGTTCGG CGATTTTGT
GTCGAACAAG GGAAGAATC GTAGACGGTC TAAGTATAAG CTTGTTCATA CCGTTAGGAC TCATAAAGGA
GCTGTTGAGA AGGCTTTCAA CTGTGTTTAC CAAGAGCAAG ATGATAATGG GAAGACCCGG GTTTCGTTGT
CGAAAGATCT TATGGCTATA GCTGGGGAAG CTCTTAAGGC GAATATCACT ACTTAGGTC CTTTGTTCT
TCCTATAAAGT GAGCAGATTG TGTTTTCAT GACTTTGGTT ACGAAGAAAC TGTTTAACTC GAAGCTGAAG
CCGTATATTC CGGATTTCAG GCTTGCGTTT GATCATTTCT GTATCCATGC TGGTGGTAGA GCTGTGATTG
ATGAGCTTGA GAAGAACTCG CAGCTTTTCG AGACTCATGT CGAGGCATCC AGAATGACAC TGCACAGATT
TGGAACACT TCTTCGAGCT CGATTTGTA TGAACCTGGCT TACATAGAGG CTAAAGGTAG GATGAAGAAA
GGAAACCGG TTTGGCAGAT TGCTTTTGGG AGTGGGTTTA AGTGTAACAG TGCAGTTTGG GTGGCTCTAA
ACAAATGTCAA GCCTTCGGTT AGTAGTCCGT GGAACACTG CATCGACCGA TATCCGGTTA AGCTCGACTT

EL5
FIGURE 11

EL5 protein sequence
Molecular Weight 60874.60 Daltons
537 Amino Acids
63 Strongly Basic(+) Amino Acids (K,R)
47 Strongly Acidic(-) Amino Acids (D,E)
198 Hydrophobic Amino Acids (A,I,L,F,W,V)
148 Polar Amino Acids (N,C,Q,S,T,Y)
9.107 Isoelectric Point
17.930 Charge at PH 7.0

SSYVRAFICT NSHKVFNFIP FFSEAMEAAN EPVNGGSVQI RTENNERRKL PNFLQSVNMK YVKLGYYHYLI
THLFKLCLVP LMAVLVTEIS RLTTDDLYQI WLHLQYNLVA FIFLSALAI F GSTVYIMSRP RSVYLVVDYSC
YLPPESLQVK YQKFMDSKL IEDFNESSE FQKILERSG LGGEETYLPEA LHCIPPRPTM MAAREESEQV
MFGALDKLFE NTKINPRDIG VLVVNCSLFN PTPSLSAMIV NKYKLRGNVK SFNLGGMGCS AGVISIDLAK
DMLQVHRNTY AVVVSTENIT QNWYFGNKA MLIPNCLFRV GGSAILLSNK GKDRRRSKYK LVHTVTRTHKG
AVEKAFNCVY QEODDNGKTG VSLSKDLMAI AGEALKANIT TLGPLVLPIS EQILFFMTLV TKKLFNSKLLK
PYIPDFKLAF DHFCIHAGGR AVIDELEKNL QLSQTHVEAS RMTLHRFGNT SSSIWYELA YIEAKGRMCK
GNRVWQIAFG SGFKCNSAVW VALNNVKPSV SSPWEHCIDR YPVKILDF

EL5
FIGURE 12

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EL6 1502 bases
TCTCCGACGATGCCCTCAGGCACCGATGCCAGAGTTCTCTAGCTCGGTGAAGCTCAAGTACGTGAACACTTGGTTACCAA
TATTGGTTAACCATTCTTTGAGTTTCTTTGATCCCGATCATGGCTATTGTCGCCGTTGAGCTTCTTCGGATGGGT
CCTGAAGAGATCCTTAATGTTTGGAAATTCACCTCCAGTTTGACCTAGTTCAGGTTCTATGTTCTTCTTCTTGTGCATC
TTCACTCTCCACTGTTTACTTTCATGTCCAAAGCCACGACCATCTACCTCGTTGACTATTCTTGTACAAAGCCACCTGTC
ACGTGTCGTGTCCTTCGCAACTTTTCATGGAAACACTCTCGTTTGATCCCTCAAGGACAAGCCCTAAGAGCGTCGAGTTC
CAAAATGAGAAATCCTTGAAACGTTCTGGCCCTCGGTGAGGAGACTTGTCCTCCCTCCGGCTATTCAATTATATTCCTCCACA
CCAAACCATGGACGCGGCTAGAAAGCGAGGCTCAGATGGTTATCTTCGAGGCCATGGACGATCTTTTCAAGAAAACCGGT
CTTAAACCTAAAGACGTCGACATCCTTATCGTCAACTGCTCTTTTCTCTCCACACCATCGCTCTCAGCTATGGTC
ATCAACAATAAAGCTTAGGAGTAATATCAAGAGCTTCAATCTTTCGGGATGGGCTGCAGCGCGGCTGATCTCA
GTTGATCTAGCCCGCACTTGCTCCAAGTTTCATCCCAATTCAATGCAATCATCGTCAGCACGGAGATCATAAAGCCT
AATTACTATCAAGGCAACGAGAGAGCCATGTTGTTACCCCAATTGTCCTTCCGCAATGGGTGCGGAGCCATACACATG
TCAAAACCGCGGCTGACCGGTGGCGAGCCAAATACAAGCTTTTCCCACTCTGTCGGGACACACCGTGGCGCTGACGAC
AAGTCTTTCTACTGTGTCTACGAAACAGGAAGACAAAGAAAGGACACGTTGGCATCAACTTGTCCAAAGATCTCATGGCC
ATCGCCGGTGAAGCCCTCAAGGCAAAATCAACCAAAATAGGTCCTTTGGTCTTACCGGCTCAGAACAACTTCTCTTC
CTACGTCCTTAATCGGACGTAAATCTTCAACCGAAATGGAACCATACATACCGGATTCAGGCTGGCCCTTCGAA
CACTTTTGCAATTCACGACGAGGACAGCGGTGATCGACGAGCTCCAAAGAAATCTACAACATATCAGGAGAACACGTT
GAGGCCCTCAAGAAATGACACTACATCGTTTGGTAACACGTCATCTTCATCGTTATGTTACGAGCTTAGCTACATCGAG
TCTAAAGGGAGAAATGAGGAGAGCGGATCGCGTTTGGCAAAATCGCGTTTGGGAGTGGTTTCAAGTGTAACCTGCGCGTG
TGGAAGTGTAACCGTACGATTAAGACACCTAAGGACGGACCATGTCGATGTAATCGACCGTTACCCCTGCTTTATT
CCCGAAGTTGTCAAACTCTA

EL6
FIGURE 13

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EL6 protein sequence
 Molecular Weight 56687.90 Daltons
 500 Amino Acids
 59 Strongly Basic(+) Amino Acids (K,R)
 46 Strongly Acidic(-) Amino Acids (D,E)
 182 Hydrophobic Amino Acids (A,I,L,F,W,V)
 127 Polar Amino Acids (N,C,Q,S,T,Y)
 8.909 Isoelectric Point
 14.567 Charge at PH 7.0

SPTMPQAPMP EFSSSVKLKY VKLGYQYLVN HFLSFLLIPI MAIVAVELLR MGPEEILNVW NSLQFDLVQV
 LCSSEFFVIFI STVYFMSKPR TIYLVYDYSY KPPVTCRVPF ATFMHSRLI LKDKPKSVFF QMRILERSGL
 GEETCLPPAI HYIPTPTMD AARSEAQMI FEAMDDLFFK TGLKPKDVIDI LIVNCSLFSP TPSLSAMVIN
 KYKLRSNIKS FNLSGMGCSA GLISVDLARD LLQVHPNSNA IIVSTEIITP NYYQGNERAM LLPNCLFRMG
 AAAIHMSNRR SDRWRACYKL SHLVTRHGA DDKSFYCVYE QEDKEGHVGI NLSKDLMAIA GEALKANITT
 IGPLVLPASE QLLFLTSLIG RKIFNPWKWP YIPDFKLAFE HFCIHAGGRA VIDELQKNLQ LSGEHVEASR
 MTLHRFGNTS SSSLWYELSY IESKGRMRRG DRVWQIAFGS GFKCNSAVWK CNRTIKTPKD GPWSDCIDRY
 PVFIPEVVKL

EL6
 FIGURE 14

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EL7 1548 bases
 ATGGACGGTGCCGGAGAAATCACGACTCGGTGGTGATGGTGGTGATGGTTCTGTTGGAGTTCAGATCCGACAAACA
 CGGATGCTACCGGATTTTCTCCAGAGCGTGAATCTCAAGTATGTGAAATTAGTTACCATTAATTAATCTCAAATCTC
 TTGACTCTCTGTTTATATCCCTCTCGCCGTTGTTATCTCCGTCGAAGCCTCTCAGATGAACCCAGATGATCTCAAACAG
 CTCGTGGATCCATCTACAATACAAATCTGGTTAGTATCATCATCTGTTCAGCGATTCTAGTCTTTCGGGTTAACGGTTTAT
 GTTATGACCCGACCTAGACCCGTTTACTTGGTTGATTCTCTTGTATTCTCCACCTGATCATCTCAAAGCTCCTTAC
 GCTCGGTTCAATGGAACAATTCTAGACTACCGGAGATTTCGATGACTCTGCTCTCGAGTTTCAACGCAAGATCCTTGAG
 CGTTCTGTTTAGGGGAAGACACTTATGTCCCTGAAGCTATGCATTATGTTCCACCGAGAAATTTCAATGGCTGCTGCT
 AGAGAAGAAGCTGAACAAGTCAATGTTGGTGCTTTAGATAACCTTTTCGCTAACACTAATGTGAAACCAAGGATATT
 GGAAATCCTTGTGTGAATTGTAGTCTCTTTAATCCAACTCCTTCGTTATCTGCAATGATTGTGAACAAGTATAAGCTT
 AGAGGTAACATTAGAAGCTACAATCTAGCGGATAGGGTTGCAGCGCGGAGTTATCGCTGTGGATCTTGTCTAAAGAC
 ATGTTGTTGGTACATAGGAACACTTATGCGGTTGTTGTTTCTACTGAGAACATTAATCAGAAATTTGGTATTTTGGTAAC
 AAGAAATCGATGTTGATACCGAACTGCTTGTTCGAGTTGGTGCTCTGCGGTTTTCGCTATCGAACAGTCGAGGGAC
 AAGAGACGGTCTAAGTACAGGCTTGATGATGATCAGGACTCACCGTGAGCAGATGATAAAGCTTTCGGTTGTGTT
 TATCAAGAGCAGGATGATACAGGGAGAACCGGGGTTTCGTTGTCGAAAGATCTAATGGCGATTGCAGGGAAACTCTC
 AAAACCAATATCACTACATTTGGTCCCTTGTCTACCGATAAGTGAGCAGATTCTCTCTTTATGACTCTAGTTGTG
 AAGAAGCTCTTTAACGGTAAGTGAAACCGTATATCCCGGATTTCAAACCTTTCGAGCATTTCTGTATCCATGCT
 GGTGGAAGAGCTGTGATCGATGAGTTAGAGAAGAACTGCGAGCTTTCACCAAGTTTCATGTCGAGGCTTCGAGGATGACT
 CTTCAATCGATTTGGTAACACATCTTCGAGCTCCATTTGGTATGAATTGGCTTACATTGAAGCGAAGGAGGATGCCGA
 AGAGGTAATCGTGTGTTGGCAAAATCGCGTTTCGGAAGTGATTTAAATGTAATAGCGGATTTGGGAAGCATTAAGGCAT
 GTGAACCTTCGAACAACAGTCTCTGGGAAGATTGTATTGACAAGTATCCGGTAACTTTAAGTTAT

EL7
 FIGURE 15

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EL7 protein sequence

Molecular Weight 57848.80 Daltons

516 Amino Acids

59 Strongly Basic(+) Amino Acids (K,R)

48 Strongly Acidic(-) Amino Acids (D,E)

189 Hydrophobic Amino Acids (A,I,L,F,W,V)

131 Polar Amino Acids (N,C,Q,S,T,Y)

8.872 Isoelectric Point

12.792 Charge at PH 7.0

MDGAGESRLG GDGGDGSVG VQIRQTRMLP DFLQSVNLKY VKLGYHYLIS NLLTCLFPL AVVISVEASQ
 MNPDDLKQLW IHLQYNLVS I ICSAILVFG LTVYVMTRPR PVYLVDFSCY LPPDHLKAPY ARFMEHSRLT
 GDFDLSALEF QRKILERSGL GEDTYVPEAM HYVPPRISMA AAREEAEQVM FGALDNLFAN TNVKKPDIGI
 LVVNCSLFNP TPLSAMIVN KYKLRCNIRS YNLGGMGCSA GVIAVDLAKD MLLVHRNTYA VVSTENITQ
 NWYFGNKKSM LIPNCLFRVG GSAVLLSNKS RDKRRSKYRL VHVRTHRGA DDKAFCVYQ EQDDTGRTGV
 SLSKDLMAIA GETLKTNITT LGPLVLPISE QILFFMTLVV KKLFNGKVKP YIPDFKLAFE HFCIHAGGRA
 VIDELEKNLQ LSPVHVEASR MTLHRFGNTS SSSIWYELAY IEAKGRMRRG NRWVQIAFGS GFKCNSAIWE
 ALRHVKPSNN SPWEDCIDKY PVTLSY

EL7

FIGURE 16

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/11384

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :AOIH 5/00, C07H 21/00; C12N 15/00, 15/82

US CL :800/205; 435/172.3; 536/23.6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 800/205; 435/172.3; 536/23.6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - Y	WO 95/15387 A2 (CALGENE INC.) 08 June 1995, especially pages 57-71.	1,9,10,18-20,22-26, 28-30 2-8,11-17,21,27
X - Y	WO 96/13582 A2 (DNA PLANT TECHNOLOGY CORP.) 09 May 1996, especially pages 33-38.	1,9,10,18,19,24,25 2-8,11-17,20-23,26-30



Further documents are listed in the continuation of Box C.



See patent family annex.

Special categories of cited documents:		"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

07 AUGUST 1998

Date of mailing of the international search report

29 SEP 1998

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/11384

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - Y	JAMES et al. Directed Tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1) Gene with the Maize Transposon Activator. The Plant Cell. March 1995, Vol. 7, pages 309-319, see especially pages 316-317.	1,9,10 ----- 2-8,11,17-30